

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 03:48:54 ; Search time 2617 Seconds
(without alignments)
14283.192 Million cell updates/sec

Title: US-10-727-010-1

Perfect score: 982
Sequence: 1 CGGCCGATCACCACATCCG.....TCGGCTCTCTGAGTAAAC 982

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	129.2	13.2	1910	AG382199	Mus muscu
C 2	127.6	13.0	1297	CG744520	P037-1-E1
C 3	127	12.9	1277	CG753585	P048-3-H1
C 4	126.6	12.9	1601	CG752479	P047-2-A0
C 5	126	12.8	1565	AG340866	Mus muscu
C 6	126	12.8	1567	CG746709	P040-1-B0
C 7	125.6	12.8	1695	CC290874	CH261-172
C 8	125.4	12.8	1874	AG448338	Mus muscu
C 9	125	12.7	2041	AG363808	Mus muscu
C 10	124.4	12.7	1107	CK162505	FGAS01510
C 11	124.4	12.7	1193	AG349830	Mus muscu
C 12	124	12.6	1471	CG748176	P042-1-A0
C 13	124	12.6	1616	CG753270	P048-2-C0
C 14	123.2	12.5	1970	CG748837	P042-4-E0
C 15	123	12.5	1087	CB908860	tr1c074xf
C 16	123	12.5	1087	CB982340	tr1c086xi
C 17	122.8	12.5	1836	AG382181	Mus muscu
C 18	122	12.4	1738	CG750956	P045-2-H0
C 19	121.6	12.4	1448	CC220110	CH261-92F
C 20	121.2	12.3	1082	CC300639	CH261-66F
C 21	121.2	12.3	1106	CB905422	tr1c074xf
C 22	121.2	12.3	1106	CF876941	tr1c074xf
C 23	121.2	12.3	1223	AG441637	Mus muscu
C 24	121.2	12.3	1258	AG441605	Mus muscu

C 25	121.2	12.3	1397	9	CL105166	ISB1-44E1
C 26	121.2	12.3	1400	6	AG429585	Mus muscu
C 27	120.8	12.3	1093	6	CB905750	tr1c075xp
C 28	120.8	12.3	1093	7	CF877401	tr1c075xp
C 29	120.8	12.3	1642	9	CG754720	P050-2-A0
C 30	120.6	12.3	1249	6	CB905420	tr1c074xf
C 31	120.6	12.3	1249	7	CF876940	tr1c074xf
C 32	120.6	12.3	1961	9	AG355522	Mus muscu
C 33	120.4	12.3	1385	9	CL044197	CH216-60G
C 34	120.2	12.2	1011	6	CB905602	tr1c075xf
C 35	120.2	12.2	1011	7	CF877292	tr1c075xf
C 36	120	12.2	1314	9	CG748456	P042-2-D1
C 37	120	12.2	1506	9	AG442117	Mus muscu
C 38	119.8	12.2	1307	9	CL647465	CH213-139
C 39	119.8	12.2	1839	9	CG747711	P041-2-B0
C 40	119.6	12.2	1204	8	CC284084	CH261-167
C 41	119.4	12.2	1008	9	AG395157	Mus muscu
C 42	119.4	12.2	1491	9	CG748472	P042-2-E0
C 43	119.2	12.1	1151	6	CB905418	tr1c074xf
C 44	119.2	12.1	1151	7	CF876938	tr1c074xf
C 45	119.2	12.1	1197	4	BI416470	haap001xa

ALIGNMENTS

RESULT 1

AG382199/c

LOCUS AG382199 1910 bp DNA linear GSS 03-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-192123.T7, genomic survey sequence.

ACCESSION AG382199
VERSION AG382199.1 GI:47993404

KEYWORDS GSS.
SOURCE Mus musculus molossinus

ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

TITLE BAC end Sequences of Library MSMg01

JOURNAL Unpublished
2 (bases 1 to 1910)

REFERENCE Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

AUTHORS Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan

TITLE 1-7-22 Suenhito-chou, Tsukuba, Ibaraki, Japan
(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/)

JOURNAL Tel: 81-45-503-9111, Fax: 81-45-503-9170
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kunita Abe (abe@tc.riken.jp).

COMMENT The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Tsukuba Institute, Bio Resource Center,
Koyada, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp

PRIMERS
Sequencing : T7
LIBRARY : PBACE3.6
Vector : R.Site 1 : BcORI.
R.Site 2 : BcORI.

FEATURES
source location/Qualifiers
1..1910
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-192123.T7"
/sex="male"
/issue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse BAC Library"

ORIGIN

Query Match	13.2%;	Score 129.2;	DB 9;	Length 1910;
Best Local Similarity	44.2%;	Pred. No. 5.1e-13;		
Matches 416;	Conservative 0;	Mismatches 523;	Indels 2;	Gaps 1

[illegible]

LOCUS

Accession	Genomic survey	Sequence
CG744520		
CG744520.1	GI:37965388	

SOURCE

REFERENCES

TITLE

JOURNAL

PUBMED

FEATURES

Best Lo

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중

Qv

Db****

QY

Db****

QY

5

2

2

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or

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ORIGIN

Query Match	13.0%;	Score 127.6;	DB 9;	Length 1297;
Best Local Similarity	42.1%;	Pred. No. 9.8e-13;		
Matches 412; Conservative	0;	Mismatches 567;	Indels 0;	Gaps 0;

[illegible]

/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

ORIGIN

Query Match	12.9%;	Score 127;	DB 9;	Length 1277;
Best Local Similarity	42.8%;	Pred. No. 1.3e-12;		
Matches 415; Conservative	0;	Mismatches 553;	Indels 2;	Gaps 1.

OY		484	GCGGCGCTCCAGACGGCGAAGGAGACAGAGGCCGCATCTTCGAGTCCGAAGGCGCTC	543
Dd		706	CCCCCCCCCCCCCCCNCCCCCCCCCCCCCCCCCCCCCCCCNNCCCCCCC	647
OY		544	CCCGTCCGCGGTGTGATCGGCACTCGAGCAACAAGCATCTCTACTCACGCG	603
Dd		646	CCCCCCCCCGNCCCCCCCCCCCCCGCCGNCCNCCCCCCCCCCCCCGCCNCCCCCCC	587
OY		604	CCTCGCGCGCCGCGGCTACTATAGGCGTTGACACATTCGCGCACTCGGCCATGGGCT	663
Dd		586	CCCCCGNCNCCCCCCCCCGCCNCCNCCCCCCCCCGCCCGCCCCCCCCCCCC	527
OY		664	CGAGGACAACGCGCTCCGCGTCCGCGCTCTCTCGGCAATCGGCTCTTGAGAACC	723
Dd		526	CCCGNCCCCCCCCCCCC	467
OY		724	CCTCATCAAAGGCGCTCATGACACGAGGCTACATGAAGAGATCTTGTGTCCAAGACTG	783
Dd		466	CCCCCCCCCCCCCCCCCCCCCCCCCGCCNCCCCCCCCCCCCCCCCCCCCCCCC	407
OY		784	GCTCTTGCGCTTCTCTCTCTACGTGACCAACAATCAATGACGTGATGSAACGGGTAAACC	843
Dd		406	CCCCCCCCCGNCCNCCCCCCCCCCCCCGCCCGNCCCCCCCCCCCCCCCCCCCC	347
OY		844	GGAACGCGATGCGCTTCATTCCGCGTCCGCGTGAATCCCGTTCTTCGCGAAGAGGGGTGCC	903
Dd		346	CCGNCNCCCGCCNCCNCCCCCCCCCCCCCCCCCGCCNCCCCCCCCCCCCCCCC	287
OY		904	GCAAGAGAACCTCGCGCGGCGATCACGDTGACCAACCGGCGCGCTTCTTCGCCGACCT	963
Dd		286	CGNNCCCGCCCCCCCCCCCCCCCCCCCCCGCCNCCCCCCCCCCCCCGCCNCCCG	227
OY		964	CCGGCGCTCTGATTTAAC	982
Dd		226	CCCCCCCCCGCCNNNNNNNC	208

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RESULT 3
LOCUS      CG753585/c
DEFINITION P048-3-H10.ya Ppa ESCRI BAC Library Pristionchus pacificus genomic,
ACCESSION  CG753585
VERSION    CG753585.1
KEYWORDS   GI:37978216
SOURCE     GSS.
ORGANISM   Pristionchus pacificus
            Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
            1 (bases 1 to 1277)
REFERENCE  Srinivasan,J., Sinz,W., Jeesse,T., Wiggers-Pereboite,L., Jansen,K.,
            Buntjer,J., van der Weulen,M. and Sommer,R.U.
            An integrated physical and genetic map of the nematode Pristionchus
            pacificus
            Mol. Genet. Genomics 269 (5), 715-722 (2003)
COMMENT    12884007
            Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            Class: BAC ends.
FEATURES   Location/Qualifiers
            1..1277
            /organism="Pristionchus pacificus"
            /mol_type="genomic DNA"
            /strain="California"
            /db_xref="taxon:54126"

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Query Match	12.9%	Score 127	DB 9	Length 1277
Best Local Similarity	42.8%	Fid. No. 1.3e-12		
Matches 415	Conservative 0	Medium 553	Indels 2	Gaps 1
QY	4	CCCGATCAACATATCTCCGAGCGCGGCTTACACCTCAACCGAGAGACATCTGCGGCTCTC	63	
DB	1268	CCCCCCCCCCCCCNCNCNCC	120	
QY	64	CGCGGCTTCTCTCGCGGCTGCGGAGTTCTTGCGCTTCGCGCAAGCCCTGCGGAGA	123	
DB	1208	CCCGCNCNCNCCCCCCCCCNCNNNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	114	
QY	124	GCGCGTGGCGGCGCTCG	183	
DB	1148	CCCCCCCCCCCCCCCCCNCNCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	108	
QY	184	CACCTTCGACATCGGCGCGGACGATGCTCTCTCGCGAGGTGTCGCGCGCGCGAGCT	243	
DB	1088	NCCNNCCCCCNCNCNCC	102	
QY	244	GCACATCGTGGCGCGCACCGGCTCTTGTTGACATCCGCGGCTCTCATGCGCTCGCTC	303	
DB	1028	CCNNCNCNCCCCCCCCCNCNNCCCCCNCNNCCCCCCCCCCCCCCCCCCCCCCCC	969	
QY	304	CGTGAAGAGCTCAACCGATTTCTTCTCGCGAGATTCAGATCGGATCGAGAGACGCG	363	
DB	968	CC	909	
QY	364	CATCGCGCGCGGATCATCAAGGTGCGACGACCGGCAAGGCGACCGCTTCAGAGCT	423	
DB	908	CNCNCCCCCCCCCNCNCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	849	
QY	424	CGTGTCAAGGCGCGCGCGCGGCTCTCTCGGCAACGCGCGTCCGAGTGAACAACGAC	483	
DB	848	CC	789	
QY	484	CGCGGCTTCCGAGCGGACGAGGCGGCGGCGGCTTCTGAGTCCGAGGCGCTCTC	543	
DB	788	CNCCCCCNCNCC	729	
QY	544	CCCGTCCGCGGTGATCGGCACTCGGACGACGACGACGACCTCTCTACTTACCTGCGC	603	
DB	728	CCCCCCCCCCCCCCCCCNCNNCCCCCNCNNCCCCCNCNNCCCCCNCNNCCCC	669	
QY	604	CCTCGCGCGCGGCGGCTACCTATCGGCTCGACATCCCGGACTCCGCGATCGGCGCT	663	
DB	668	CCCCCCCCCCCCCNCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	609	
QY	664	CGAGGACAAAGCGCTCGGCGTCCGCGCTCTCGGACATCGGCTCTGAGACAGCGCGCT	723	
DB	608	CCCCCCCC--CCCCCNCNCCCCCCCCCCCCCNCNCCCCCCCCCCCCCCCCCCCC	551	
QY	724	CCTCATCAAGGCTCTCATCGACGAGGCTACATGAAGAGATCTCTGTCTCAAGCATG	783	
DB	550	CCCCCCCCCCCCCCCCCNCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	491	
QY	784	GCTCTTGGGCTTCTCTCTGATGTAACAACATCATGAGCGTGAAGGACGCGGTGAAC	843	
DB	490	CC	431	
QY	844	GGACGAGATGAGCTTATCCGAGCTCGCGTGAATCCGCTTCTCGGAGAAAGGCGTGC	903	
DB	430	CC	371	
QY	904	GAGAGAGACCTTGGCGGAGTACCGGTACCAACCCGCGCGGCTTCTTCCCGACCT	963	
DB	370	NCCCCCCCCCCCCCCCCCCCCCCCCCNCNCCCCCNCNCCCCCNCNCCCCCCCCCCCC	311	

Qy 964 CCGGCGCTCC 973
Db 310 CCCCCCCCCC 301

RESULT 4
CG752479/c 1601 bp DNA linear GSS 24-OCT-2003

LOCUS P047-2-A01.2a Ppa Scori BAC Library Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CG752479
VERSION CG752479.1 GI:37975985

KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 1601)
AUTHORS Buntjer, J., van der Meulen, M. and Sommer, R. J.
Srinivasan, J., Sinz, W., Jeease, T., Wiggers-Perebolte, L., Jansen, K.,
An integrated physical and genetic map of the nematode Pristionchus pacificus

JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE 22835951
PUBMED 12884007

COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de

FEATURES
source Class: BAC ends.
Location/Qualifiers

1. 1601
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_11b="Ppa Scori BAC library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

ORIGIN

Query Match 12.9%; Score 126.6; DB 9; Length 1601;
Best Local Similarity 41.5%; Pred. No. 1.5e-12;
Matches 402; Conservative 0; Mismatches 567; Indels 0; Gaps 0;

Qy 4 CCGGATCACATCTTCGAGGCGGCTTACCTTACCCAGACGACATCTGGGCTCTC 63
Db 1250 CCCCCCCCCCCCCCCCCCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 1191
Qy 64 CGCGGCTTCTCGGCGGCTGCGGAGTTCTTGGCTCCCGAAGGCTTGGCGAAGA 123
Db 1190 NCCCCCNCCNCC 1131
Qy 124 GCGCGTGGCGGAGCTTCGCGCGGCGCGCGCGCGCGCTGCGACATCTGAGAGTGC 183
Db 1130 CC 1071
Qy 184 CACCTTGACATCGGCGCGGAGTGTCTCTCTCGCGAGGTGTCGCGCGCGCGAGT 243
Db 1070 CCCCCCCCCCCCCCCCCCNCCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCN 1011
Qy 244 GCAATCTGGCGCGGACCGGCTTGTGTGACCCGCGGCTCTCATGCGCTCTCGTC 303
Db 1010 CCCCCCCCCCCCCCCCCCCCCCNCCCCCCCCCCCCCCCCCCCCCCCCCCCC 951
Qy 304 CGTGAAGAGCTCAACCATCTTCTCTCGCGAGATTCAGTACGAGATCGAGACACCG 363
Db 950 CCNCCNCC 891

Qy 364 CATCCGCGCGGCGATCATCAAGGTGACCAACGAGGACACCCCGTTCCAGAGACT 423
Db 890 CCCCCCCCCCCCCCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCN 831
Qy 424 CTTGCTCAAGGCGCGCGCGGCTTCTGCGACCGGCTGCGGATACCAACAC 483
Db 830 CCCCCNNCNCNCCCCCCCCCCCCCCCCCCCCNNCCCCNNCCCCCCCCCCCC 771
Qy 484 CGCGGCTTCCGAGCGACGAGCGAGACGAGGCGGCGCATCTTGAAGGCGCTTC 543
Db 770 CCGNCCNCCCNCCC 711
Qy 544 CCGTCCGCGGTGATCGGCGCATCTCGACGACGACGACGACCTTCTTCACTACCG 603
Db 710 CCGNCCNCCCCCCCCCCCCCNCCCCCCCCCCCCCCCCCCCCNNCCCCCCCC 651
Qy 604 CTTGCGCGCGCGGCTTACCTCATCGGCTTGCACATCGCGGACCTCGGCTT 663
Db 650 CCCCCCCCCCCCCCCCCCNCCCCCCCCCCCCCCCCCCCCNNCCCCCCCC 591
Qy 664 CGAGGACACGCGCTTCGCGGCTTCCTGCGATCGGCTTCTGAGAGACCGGCGCT 723
Db 590 CCCNNCCNCCCC 531
Qy 724 CTTGATCAAGGCGCTTATCGACGAGGCTACATGAAGAGATCTCTGTCTCAAGACTG 783
Db 530 CCGCCNCCNCCCCCCCCCCCCNNCCNCCCCCCCCCCCCCCCCCCCCNNCCC 471
Qy 784 GCTTTGGGCTTCTTCCTCTATCGGACCAACATGAGAGTGAACCGCGGAAACC 843
Db 470 CCCCCNCCNCCCCCCCCCCCCCCCCCCCCNNCCCCCCCCCCCCCCCCCCCC 411
Qy 844 GAGCGGATGCGCTTCAATCCGCTTCGCGGTGATCCGTTCTCCGAGAGAGGCGTGC 903
Db 410 CCCCCCCCCCCCCCCCCCNCCNCCCCCCCCNNCCNCCNCCNCCCCCCCC 351
Qy 904 CGAGGAGACCTTCGCGGCGATCACGTTGACCAACCGGCGCTTCTTCCGACCTT 963
Db 350 CCCCCNCCNCCCCCCCCCCCCCCCCCCCCCCCCNNCCNCCNCCCCCCCC 291
Qy 964 CCGGCGCTC 972
Db 290 CCCCCCCCC 282

RESULT 5
AG340866 1565 bp DNA linear GSS 02-JUN-2004
LOCUS Mus musculus molossinus DNA, clone:MSMg01-134A20.TU, genomic survey sequence.

ACCESSION AG340866
VERSION AG340866.1 GI:47914176
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1565)
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan

COMMENT (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

PRIMERS

Sequencing : TU

LIBRARY

Vector : pBACE3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

FEATURES

source location/Qualifiers

1..1565

/organism="Mus musculus molossinus"

/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMg01-134A20.TU"

/sex="male"

/tissue_type="mixture of kidney and spleen"

/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 12.8%; Score 126; DB 9; Length 1565;

Best Local Similarity 42.4%; Pred. No. 1.9e-12;

Matches 411; Conservative 0; Mismatches 559; Indels 0; Gaps 0;

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4  CCGATCAACATCTCCAGAGCGGCTTCACTCAACCCAGAGCAATCTGGGCTCTC
456  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
64  CGCGGCTTCTCGCGGCTTGCGAGTCTTCTTGAGCTCCGCAAGGCTTGGCGAGA
516  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
124  GGGCGTGGCGGCGCTCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
576  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
184  CACTTTCACATCGAGCGCGAGTCTCTCTCGCGAGTGTCCGCGCGCGCGAGT
636  NCCGNCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
244  GCACATCGTGGCGCGACCGGCTTGTGTGACCCCGCGCTTCTCGAGGCTTCTG
696  CCGGNNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
304  CGTGAAGAGTCAACCACTTCTCTCGCGAGATCCAGTACGCGATGAGAGACCG
756  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
364  CATCGCGCGGATCATCAAGTGGACGACACCGGCAAGGCAACCGGTTCCAGAG
816  CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
424  CGTGTCAAGGCGCGCGCGCGCGCGCTCTCTCGCAACCGCGGTGACCAACCA
876  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
484  CGCGGCTTCTCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
936  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
544  CCGGCGCGCGGTGTGATCGGCGCACTCGAGGACCAACCGGCACTTCTTCAAC
996  CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
604  CCGGCGCGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
1056  CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
664  CGAGAGCAACGCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
1116  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
1175  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

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QY 724 CCTGATCAAGGCGCTCATGACCAAGGCTACATGAGAGATCTGTCTCAAGCATG 783
DB 1176 CCCCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1235
QY 784 GCTCTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 843
DB 1236 NCCCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1295
QY 844 GAGCGCATGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 903
DB 1296 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1355
QY 904 GCAGAGACCTCTCGCGGATCAACCGTGAACCAACCGCGCGCTTCTCTCTCTCT 963
DB 1356 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1415
QY 964 CCGGCGCTCTC 973
DB 1416 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1425

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RESULT 6

CG746709/c 1567 bp DNA linear GSS 24-OCT-2003

LOCUS P040-1-B08.2a Ppa EcoRI BAC Library Pristionchus pacificus genomic, 1567 bp

DEFINITION genomic survey sequence.

ACCESSION CG746709

VERSION CG746709.1 GI:37967635

KEYWORDS GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

REFERENCE Srinivasan,J., Sinz,M., Jeeze,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J. An integrated physical and genetic map of the nematode Pristionchus pacificus

1 (bases 1 to 1567)

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

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Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

Neodiplogasteridae; Pristionchus.

FEATURES

source location/Qualifiers

1..1567

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Ppa EcoRI BAC Library"

/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

ORIGIN

Query Match 12.8%; Score 126; DB 9; Length 1567;

Best Local Similarity 40.1%; Pred. No. 1.9e-12;

Matches 390; Conservative 0; Mismatches 583; Indels 0; Gaps 0;

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QY 1 CGGCGGATCAACATCTCCAGAGCGGCTTCACTCAACCCAGAGCAATCTGGGCTC 60
DB 1487 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1428
QY 61 CTCGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 1427 NCNCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368

```


Oy	605	TTGGCGCGCGGGGTACCTGATGGAGCTGGACCAACATCCGGACCTCGCATGGAGCTC	664
Db	926	CCNCCGGCCC-----CCCCCCCCCNCGCCCCCCCCCNCCCCCCCCCGCCCCCCCCCCCCC	981
Oy	665	GAGGACAAACGCTTCGCGAGCTCGAGCCTCTCTCGGACATCGCTCTGGCAACCCGGAGCCTC	724
Db	982	CCGGCCCCCCCCCGGCGCGCCCCCCCCCCCCCCCCCCCCCGCCCCCNCGCCCCCNCCG	1041
Oy	725	CTCATCAAGGCTTCATGACCAAGGGCTACATGAAGCAGATCTTCGTGTCAACGACTGG	784
Db	1042	CCCCCNCCNCCCCCGCGCCCCCCCCCCCCCCCCCGCCCCCGCCCCCCCCCCCCC	1101
Oy	785	CTCTTCGGCTTCTCTCTCTAGCTGACCAACATCATGACGATGAGACGGGTGAACCCG	844
Db	1102	CCCCGCCCCCCCCCCCCCNCCGNCGCGCGCCCCCCCCCGCCCCCCCCCGAGCCCC	1161
Oy	845	GACGCGATGAGCTTTCATCCGCGCTCCGCGTGAATCCGTTCTTCGCGAAGAGGCGTGGC	904
Db	1162	CCCCCCNCGCCCCCGNCCGCGCGCGCGCGCGCGCGCGCCNCGCGCCCCCCCCCNCGCCCN	1221
Oy	905	CAGAGACCTTCGCGCGGATACCGGTGACCAACCGGAGCGGCTTCTCTCCCGACCTTC	964
Db	1222	CGCCCGCCNCCCCCCCCCGCGGCCCCCGGCGCGCCCCCCCCCCCCCNCCGCGCCCC	1281
Oy	965	CGCGGCTTC	973
Db	1282	CGCCCCCCC	1290

RESULT 8			
AG448338/c			
LOCUS	AG448338	1874 bp	DNA linear
DEFINITION	Mus musculus molossinus DNA, clone:MSWg01-332E03.TU, genomic survey sequence.		GSS 03-JUN-2004

ACCESSION	ACA48338
VERSION	ACA48338.1
KEYWORDS	GSS.
SOURCE	Mus musculus molossinus
ORGANISM	Mus musculus molossinus

REFERENCE	1
AUTHORS	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE	BAC end Sequences of Library MSW01
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1874)
AUTHORS	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (17-NOV-2003) Maehara Hattori, The Institute of Physical

COMMENT

Clones are derived from the mouse BAC library MSNG01. For BAC library availability, please contact Kuniya Abe (abe@crc.riken.jp), Tsukuba Institute, Bio Resource Center
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyada, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@crc.riken.jp

FEATURES
SOURCE

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Location/Qualifiers
1. 1874
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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/clone="MSMG01-332B03.TU"
/sex="male"
/tissue type="mixture of kidney and spleen"
/clone_lib="MSMG01 Mouse Male BAC Library"

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Query Match	12.8%;	Score 125.4;	DB 9;	Length 1874;
Best Local Similarity	41.3%;	Pred. No. 2.4e-12;		
Matches 402;	Conservative 0;	Mismatches 571;	Indels 0;	Gaps 0;

[illegible]

Oy	961	CCTCGGGGCTTC	973
Dd	862	CCCCCCCCCCC	850
RESULT 9			
LOCUS	AG363808		
DEFINITION	Mus musculus molossinus DNA, clone:M5Mg01-165M06.TU, genomic survey	2041 bp	DNA linear GSS 03-JUN-2004
ACCESSION	AG363808		
VERSION	AG363808.1	GI:47975013	
KEYWORDS	GSS.		
SOURCE	Mus musculus molossinus		
ORGANISM	Mus musculus molossinus		
REFERENCE	Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.		
AUTHORS	BAC end Sequences of Library M5Mg01		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 2041)		
REFERENCE	Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.		
AUTHORS	Direct Submission		
TITLE	Submitted (17-NOV-2003) Maashira Hattori, The Institute of Physical		
JOURNAL	and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan		
	1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
	(E-mail:hattori@gsc.riken.jp, URL:http://hgpc.gsc.riken.go.jp/,		
	Te1:81-45-503-9111, Fax:81-45-503-9170)		
	Clones are derived from the mouse BAC library M5Mg01. For BAC		
	library availability, please contact Kunihya Abe (abe@rtc.riken.jp.)		
	Tsukuba Institute, Bio Resource Center,		
	The Institute of Physical and Chemical Research (RIKEN) 3-1-1		
	Koyadai, Tsukuba, 305-0074 Japan		
	phone: 81-298-36-9189, fax: 81-298-36-9199		
	e-mail: abe@rtc.riken.jp		
COMMENT	PRIMERS		
	Sequencing : TJ		
	LIBRARY		
	Vector : pBACe3.6		
	R.Site 1 : EcoRI		
	R.Site 2 : EcoRI.		
FEATURES	Location/Qualifiers		
source	1..2041		
	/organism="Mus musculus molossinus"		
	/mol_type="genomic DNA"		
	/sub_species="molossinus"		
	/db_xref="taxon:57486"		
	/clone="M5Mg01-165M06.TU"		
	/sex="male"		
	/issue_type="mixture of kidney and spleen"		
	/clone_lib="M5Mg01 Mouse Male BAC Library"		
ORIGIN			
Query Match	12.7%	Score 125;	DB 9; Length 2041;
Best local Similarity	46.9%;	Pred. No. 2.8e-12;	
Matches 460;	Conservative 0;	Mismatches 515;	Indels 6; Gaps 2;
Oy	1	CGGCCCATCAATCTCCGAAGCCGGGTTCACCTTACCCACGACGACATCTGGGGCTC	60
Dd	881	CCGCCCGCCCGCCGCACCGCCCCCGCCGCGCGCCCGCCCCCCCCCCCCCGCC	940
Oy	61	CTCGCCGCGGCTTCCTCCGCGCGCTGCGCGAAGTTTGAGCTCCGCGAAGGCGCTGCGCGA	120
Dd	941	CCCCGCGCGGCGCCCG	1000
Oy	121	GAAGCGCGTGGCGGCGCTCCG	180
Dd	1001	GCG	1060
Oy	181	GTCACATTGACATCGGCGCGCGCGCGCTCTCTCTCGCGGAGGTGTCCC-----GCGCC	235

[illegible]

TITLE Functional Genomics of Abiotic Stress in Wheat and Canola Crops
JOURNAL Unpublished (2003)
COMMENT Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas.est@cs.usask.ca

This sequence is the direct result of the base calling software
phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [3,186].
Plate: L4B005 row: C column: 12.

FEATURES
source location/Qualifiers
1..1107
/organism="Triticum aestivum"
/mol_type="rRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: library 4 Gate 8"
/note="Organ: Crown and leaf; Vector: PCMV.SPORT6;
Conditions for growth: Seeds were germinated in a
water-saturated mix (50% black earth and 50% Promix) in a
growth chamber for 7 days under an irradiance of 200 mmol
m-2 sec-1. The temperature was maintained at 20 degrees C
with a 15-hr photoperiod under a relative humidity of 70%.
After this period watering of plants was stopped. Four
time points were sampled during a two week period; the
first after wilting was observed and the last, two weeks
later, consisted of live crown and leaf tissue (leaf
tissue that was yellow was not included in sampled
material). First strand synthesis in this library was done
in the presence of methylated dCTP thereby protecting from
internal cleavage with NotI."

ORIGIN

Query Match 12.7% Score 124.4; DB 7; Length 1107;
Best Local Similarity 39.7%; Pred. No. 3.6e-12;
Matches 384; Conservative 0; Mismatches 581; Indels 3; Gaps 1;

6 CGATCACCATTCCGAGCGCGCTTCAACCCACGACGACATCTGCGCTCTCCG 65
123 GCGGACAGCTTCTCGGCTCTCTGCGAGCTCATCTGCTCCCGCGGACGCGCC 182
66 CCGGCTCTCTCGGCTCTGCGGAGTCTTCTGCGCTCCGCAAGGCTCTGCGGAAAG 125
183 CCGGCTCTCTCGGCTCTGCGGAGTCTTCTGCGCTCCGCAAGGCTCTGCGGAAAG 242
126 CCGGCTCTCTCGGCTCTGCGGAGTCTTCTGCGCTCCGCAAGGCTCTGCGGAAAG 185
243 GCGGAGGAGGCG 302
186 CTTTGACATCTCGGCGCGGAGTCTCTGCGGAGTGTCTCCGCGCGCGCGGAGTGC 245
303 NNNNNCCCCCGCCG 362
246 ACATGCTGCG 305
363 CCNCG 422
306 TGGAGAGGTCAACGAGTCTTCTCTGCGGAGATTCAGTACGAGATTCAGGACACCGGA 365
423 CCG 482
366 TCG 425
483 CCG 542
426 TCGTCAAGGCG 485
543 CCG 602

QY 486 CCGCTCCGACGCGAGGCGAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 545
DB 603 CCG 662
QY 546 CCGCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 605
DB 663 NNNCG 719
QY 606 TCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 665
DB 720 NNNCG 779
QY 666 AGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 725
DB 780 NNNCG 839
QY 726 TCGTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 785
DB 840 CCG 899
QY 786 TCTTGGCTTCT 845
DB 900 CCG 959
QY 846 ACGGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 905
DB 960 CCG 1019
QY 906 AGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 965
DB 1020 CCG 1079
QY 966 GCGGCTTC 973
DB 1080 CCG 1087

RESULT 11

AG349830/c

LOCUS 1193 bp DNA linear GSS 02-JUN-2004
DEFINITION Mus musculus moJossinus DNA, clone:MSMg01-146D19.T7, genomic survey
sequence.

ACCESSION AG349830
VERSION AG349830.1 GI:47923140

KEYWORDS GSS.
SOURCE Mus musculus moJossinus

ORGANISM Mus musculus moJossinus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC and Sequences of Library MSMg01

AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE BAC and Sequences of Library MSMg01

JOURNAL Unpublished
2 (bases 1 to 1193)

REFERENCE Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan

COMMENT (E-mail: hattori@riken.jp, URL: http://bgr-gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@r.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@r.riken.jp

PRIMERS
Sequencing : T7
Library
Vector : pBAC3.6

R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. .1193
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="WSMg01-146D19.T7"
/sex="male"
/issue_type="mixture of kidney and spleen"
/clone_lib="WSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 12.7%; Score 124.4; DB 9; Length 1193;
Best Local Similarity 40.0%; Pred. No. 3.6e-12;
Matches 388; Conservative 0; Mismatches 578; Indels 4; Gaps 1;
4 CCGGATCAACATCTCCGAGGCGGCTTACCTGACCCGACGACATCTGGGCTCTC 63
1151 CC 1092
64 CCGCGCTTCTCTCCGCGCTGAGCGGAGTTCTTGGGCTCCGCAAGCGCTTGGCGAGA 123
1091 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1032
124 GCGCGTGGCGGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 183
1031 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 972
184 CACCTTGCACATCGGCGGAGCGTGTCTCTGCGAGGTCGCGCGCGCGCGAGCT 243
971 CC 912
244 GCACATCGTGGCGGCGGCGGCGGCTGTGTTGACCGCGGCTCTCATGCGGCTCGGTC 303
911 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 852
304 GGTGAGAGAGCTGACCGAGTTTCTTCTCGGAGATTCAGTACGCGCATGAGAGACCGG 363
851 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 792
364 CATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 423
791 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 732
424 GGTGCTCAAGGCGGCGGCGGCGGCTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 483
731 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 672
484 GCGCGCTTCCGAGCGGAGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 543
671 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 612
544 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 603
611 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 556
604 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 663
555 NNNNNCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 496
664 CGAGGAGCAAGCGCTTCCGCGGCGGCTCTCTGCGGCGGCTCTTGGAGAGCGCGGCGCT 723
495 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 436
724 CCTCATCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 783
435 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 376
784 GCTCTTGGGCTTCT 843
375 NNNNNCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 316

QY 844 GAGCGGAGTGGCTTATCCCGCTCCGGGTATCCCGTCTCCGCGAGAGAGGCGTCC 903
DB 315 NNNNNCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 256
QY 904 GAGAGAGACCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 963
DB 255 NCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 196
QY 964 CCGGCGGCTCC 973
DB 195 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 186

RESULT 12
CG748176 1471 bp DNA linear GSS 24-OCT-2003
LOCUS CG748176
DEFINITION P042-1-A01.za Ppa EcoRI BAC Library Pristionchus pacificus genomic.
ACCESSION CG748176
VERSION CG748176.1 GI:37969102
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Nemodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 1471)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buitjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
JOURNAL
MEDLINE
PUBMED
12884007

COMMENT
Contact: Sommer RJ
Evolunatory Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES

source
1. .1471
Location/Qualifiers
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN

Query Match 12.6%; Score 124; DB 9; Length 1471;
Best Local Similarity 42.0%; Pred. No. 4.2e-12;
Matches 409; Conservative 0; Mismatches 564; Indels 0; Gaps 0;
1 CCGGCGGATCAACATCTCCGAGGCGGCTTACCTGACCCGACGAGACATCTGGGCTC 60
DB 186 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 245
QY 61 CTTCGCGGCTTCTCTCCGCGCTGCGGAGTTCTTGGGCTCCGCAAGGCGCTTGGCGA 120
DB 246 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 305
QY 121 GAAGCGGCTGCGGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 306 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 365
QY 181 GTCACCTTGCACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 366 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 425

QY 721 CCTCTCATGAGGCGCTTATGACGAGGCTAATGAAGCATCTTGTGTCCAACGA 780
Db 770 CCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 711
QY 781 CTGGCTTCTGAGCTTCTCTCTCTAGACGAACATCATGAGCGTATGAGCGGATGA 840
Db 710 CCC 651
QY 841 CCGGAGGAGATGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db 650 CCC 591
QY 901 GCGGAGAGAGATGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db 590 CCCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 531
QY 961 CTTCCGCGCTCC 973
Db 530 CCCCCCCCCCCCC 518

RESULT 14
CG748837/c 1970 bp DNA linear GSS 24-OCT-2003
LOCUS P042-4-E01.za Ppa EcORI BAC Library Pristionchus pacificus genomic,
DEFINITION genomic survey sequence.
ACCESSION CG748837
VERSION CG748837.1 GI:37969763
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Nemodiplogasteridae; Pristionchus.
1 (bases 1 to 1970)
Srinivasan,J., Sinz,W., Jeease,T., Wiggers-Perrebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
22835951
12884007
JOURNAL
MEDLINE
PUBMED
COMMENT

TITLE
AUTHORS
REFERENCE
JOURNAL
MEDLINE
PUBMED
COMMENT
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Classes: BAC ends.
Location/Qualifiers
1..1970
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcORI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

FEATURES
source
1..1970
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcORI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN
Query Match 12.5%; Score 123.2; DB 9; Length 1970;
Best Local Similarity 38.1%; Pred. No. 5.8e-12;
Matches 360; Conservative 0; Mismatches 583; Indels 2; Gaps 1;

QY 31 CACCTTACACGAGGACATCTGCGGCTCTCGGCGGCTTCTCTCGGCGGCTGCGCGGA 90
Db 1581 CCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 1522
QY 91 GTTCTTGGGCTCCGCAAGGCGCTCGCGGAGAGGCGGCGGCGCTCTCGGCGGCGCG 150
Db 1521 CCC 1462

QY 151 CCGCGCGGCGCTGCGCACATCTGAGAGTGTCCACTTTCAGCATCTGCGCGGCGAGCTGT 210
Db 1461 CCC 1402
QY 211 CTTCTGCGGAGAGTGTGCGGCGCGGCGGAGTG--CAGCATCTGAGCGGCGGCGCTC 268
Db 1401 CCC 1342
QY 269 TGGTTGACCGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 328
Db 1341 NCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 1282
QY 329 CTTCGCGAGATCTAGTATGAGATGAGAGACCGGATCTCGCGCGGCGGATATCAAGTG 388
Db 1281 CCC 1222
QY 389 GCGACACCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 448
Db 1221 NCC 1162
QY 449 TCCCTGCGCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 508
Db 1161 CCC 1102
QY 509 CAGCAGCGCGCATCTTCTGAGTCCGAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 568
Db 1101 NCC 1042
QY 569 TCCGACGACGAG 628
Db 1041 CCC 982
QY 629 GAGCTTGCACATCTCTGCGCATCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 688
Db 981 CCC 922
QY 689 CTCTCTGAGCATCT 748
Db 921 CCC 862
QY 749 GGTCTATGAGAGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 808
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QY 809 ACACAATCATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
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Db 681 CCC 637

RESULT 15
CB908860/c 1087 bp mRNA linear EST 02-JUL-2003
LOCUS trico86x120 T.reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone trico86x120, mRNA sequence.
ACCESSION CB908860
VERSION CB908860.1 GI:30123518
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 1087)
Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuer,F., Houlek,T.D., England,G.J.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchellson,C.,

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 04:49:55 ; Search time 462 Seconds
(without alignments)
12541.670 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
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- 21: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	982	100.0	982	US-10-727-010-1	Sequence 1, Appli
2	982	100.0	1082	US-09-881-165-4	Sequence 4, Appli
3	628	64.0	3713	US-10-272-351-29	Sequence 29, Appli
4	624.6	63.6	1029	US-09-791-138A-3	Sequence 3, Appli
5	566.8	57.7	1071	US-10-477-469-6	Sequence 6, Appli
6	566.8	57.7	1155	US-10-477-469-5	Sequence 5, Appli
7	565.2	57.6	1155	US-10-477-469-8	Sequence 8, Appli
8	562	57.2	1155	US-10-477-469-7	Sequence 7, Appli
9	167.4	17.0	978	US-10-282-122A-25658	Sequence 25658, A
10	166.4	16.9	981	US-10-282-122A-28172	Sequence 28172, A
11	148.8	15.2	918	US-10-282-122A-26226	Sequence 26226, A

C	12	136.2	13.9	985	18	US-10-363-345A-31407	Sequence 31407, A
C	13	136.2	13.9	985	18	US-10-363-345A-31408	Sequence 31408, A
C	14	122.6	12.5	1296	17	US-10-398-221-610	Sequence 610, App
C	15	122.6	12.5	1311	17	US-10-398-221-613	Sequence 613, App
C	16	122.6	12.5	319630	17	US-10-398-221-613	Sequence 7, Appli
C	17	122.6	12.5	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
C	18	119.2	12.1	65140	18	US-10-203-295-1	Sequence 1, Appli
C	19	119.2	12.1	125401	18	US-10-203-295-35	Sequence 35, Appli
C	20	117.4	12.0	2712	17	US-10-282-122A-24663	Sequence 24663, A
C	21	116.8	11.9	85692	17	US-10-461-194-1	Sequence 1, Appli
C	22	115.6	11.8	1773	15	US-10-156-761-6199	Sequence 6199, Ap
C	23	115.6	11.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
C	24	114.8	11.7	88400	18	US-10-844-716-1	Sequence 1, Appli
C	25	112.6	11.5	2731748	18	US-10-297-465A-1	Sequence 1, Appli
C	26	112.6	11.5	2731748	18	US-10-297-465A-1	Sequence 47969, A
C	27	111.4	11.3	3088	18	US-10-437-963-47969	Sequence 4, Appli
C	28	110.8	11.3	1208	18	US-10-716-803-4	Sequence 1, Appli
C	29	110.8	11.3	5392	18	US-10-716-803-1	Sequence 53, Appli
C	30	109.6	11.2	1377	16	US-10-214-446-53	Sequence 20, Appli
C	31	109.6	11.2	4466	10	US-09-940-316B-20	Sequence 16, Appli
C	32	109.6	11.2	4478	10	US-09-940-316B-22	Sequence 22, Appli
C	33	109.6	11.2	4571	10	US-09-940-316B-18	Sequence 18, Appli
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C	39	107.6	11.0	969	18	US-10-363-345A-26084	Sequence 6190, Ap
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C	42	106.6	10.9	1796	18	US-10-437-963-43317	Sequence 47, Appli
C	43	106.6	10.9	12733	14	US-10-032-393-47	Sequence 8, Appli
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ALIGNMENTS

RESULT 1
US-10-727-010-1
; Sequence 1, Application US/10727010
; Publication No. US20040250298A1
; GENERAL INFORMATION:
; APPLICANT: Pinkerton, T. Scott
; APPLICANT: Howard, John A.
; APPLICANT: Wild, Jim R.
; TITLE OF INVENTION: Methods for Selecting and Screening for Transforms
; FILE REFERENCE: P05574US01
; CURRENT APPLICATION NUMBER: US/10/727,010
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/430,626
; PRIOR FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 982
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence originally obtained from Flavobacterium sp., Genbank
; OTHER INFORMATION: accession number M29593. Sequence translated and back-translated
; OTHER INFORMATION: with BACKTRANSLATE (Misc. GCG, ver. 9). Deleterious sequences
; OTHER INFORMATION: removed with FINDPATTERN (Misc. GCG, ver. 9).
US-10-727-010-1

Query Match 100.0%; Score 982; DB 18; Length 982;
Best Local Similarity 100.0%; Pred. No. 1e-210;
Matches 982; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CGCCGCATCACCATTCTCCGAGCGCGCTTACCTCACCACGACACATCTCGCGCTC 60

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QY 181 GTGCACTTTCGACATCGGCGCGAGCGTGTCTCTCGCGCGAGTGTCCGCGCGCGCGA 240
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QY 361 CGGCACTCGCGCGCGCATCATCAAGGTGCGACACCGCGCAAGCGCACCGCTTCCAGGA 420
Db 361 CGGCACTCGCGCGCGCATCATCAAGGTGCGACACCGCGCAAGCGCACCGCTTCCAGGA 420
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RESULT 2

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US-09-881-165-4
; Sequence 4, Application US/09881165
; Publication No. US20020039772A1
; GENERAL INFORMATION:
; APPLICANT: HOOD, ELIZABETH
; APPLICANT: HOWARD, JOHN
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; APPLICANT: BAILEY, MICHELE
; APPLICANT: GASTEL, FRANS VAN
; APPLICANT: WANG, HUANG
; APPLICANT: WARD, MICHAEL
; APPLICANT: WOODARD, SUSAN
; TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
; ENZYMES PRODUCED IN PLANTS
; FILE REFERENCE: 10032R
; CURRENT APPLICATION NUMBER: US/09/881,165
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/211,732
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding
; US-09-881-165-4
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Query Match 100.0%; Score 982; DB 9; Length 1082;

Best Local Similarity 100.0%; Pred. No. 1e-210; Matches 982; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 461 CGGATCGCGCGCGCATCATCAAGGTGCGACACCGCGCAAGGCGCACCGCTTCCAGGA 420
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QY 601 CGCGCTGCGCGCGCGCGCGCTCATCGGCGCTTCAAGCGAGACCGAGACCGCGCATCG 660
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RESULT 3

US-10-272-351-29
; Sequence 29, Application US/10272351
; Publication No. US20040005673A1
; GENERAL INFORMATION:
; APPLICANT: Jarell, Kevin
; APPLICANT: Turczyk, Brian
; TITLE OF INVENTION: System for Manipulating Nucleic Acids
; FILE REFERENCE: 2003320-0013
; CURRENT APPLICATION NUMBER: US/10/272,351
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 29
; LENGTH: 3713
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Presents the
US-10-272-351-29

Query Match 64.0%; Score 628; DB 17; Length 3713;
Best Local Similarity 77.9%; Pred. No. 1.5e-131;
Matches 757; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

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Db 139 CGGCTCATCAATCTCTGAAGCGGCTTTCACACTGATCTCAAGACATCTGCGGCGAG 198
Qy 61 CTCGCGCGGCTTCTCTCCGCGCTTCGCGAGATTTCTTGCGCTCCGAGAGCGCTCGCGA 120
Db 199 CTCGCGAGGATTTCTGCGGCTTTCGCGAGATTTCTTGCGAGCGGAGAGCTTACGCGA 258
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Qy 181 GTTCACTTTCGACATGCGCGCGCGAGGTCCTCTCCGCGCGAGGTCCTCCGCGCGCGCG 240
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Qy 241 CGTGCATCATCTGCGCGCGCGAGCGGCTTCGTTGACCGCGCGCTTCGATGCGGCTCGG 300
Db 379 CGTTCATATCTGCGCGCGCGAGCGGCTTCGTTGACCGCGCGCTTCGATGCGGATGAG 438
Qy 301 CTCGCGAGAGACTTACCAAGTTCTTCTCCGCGAGATTCGATAGGCGATGAGAGAC 360
Db 439 GAGTGAAGAGAACTCAACAGTTCTTCTCCGCGCGAGATTCATATGCGATGAGAGAC 498

Qy 361 CGGATCCGCGCGGATCATCAAGTGGCCACACCGGAGAGGACCCCGTTCCAGGA 420
Db 499 CGGATTTAGGCGGCGCATTTATAGTGGCCACACAGGAGAGGAGCCCTTTCAAGA 558
Qy 421 GCTGTGCTCAAGGCGCGCGCGCTTCCTTCGCGACCGGCGTGGCGTGAACCA 480
Db 559 GTTATGTTAAAGCG 618
Qy 481 CACGCGCGCTCCGCGCGGACGAGGAGGCGCGCATCTTGAATCCGAGGCGCT 540
Db 619 CACGCGAGAGATCAAGCGCGAGTGTAGACAGAGGCGCGCATTTTGAATCCGAGGCTT 678
Qy 541 CTCGCGCTCCGCGGCTGATGACGCGACTCGACGACGACGACGACGACGACGAC 600
Db 679 GAGCGCGCTCAAGGCTTTTATTTGATCAAGGATATATCTAGCATTTGAGTATCTGA 738
Qy 601 CGGCTTCGCGCGCGCGGCTTACATGAGGCTTCGACGACGACGACGACGACGAC 660
Db 739 CGGCTTCGCGCGCGGATACCTCATGATGATGATGATGATGATGATGATGATG 798
Qy 661 CCTGAGAGACACGCTCCGCGTCCGCGCTCCGCGGATCCGCTCCGCGAGACCGCG 720
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Qy 721 CCTCTCATCAAGGCGCTCATGACAGGCGCTACAGAGATCTCTGTTCCAGCA 780
Db 859 TCTCTTATCAAGGCGCTCATGACAGGCGCTACAGAGATCTCTGTTCCAGATGA 918
Qy 781 CTGGCTCTTCGCGCTTCTCTCTAGTGACCAACATCATGAGATGAGACCGGCTGA 840
Db 919 CTGGCTCTTCGCGCTTCTCTCTAGTGACCAACATCATGAGATGAGATGCGGTGA 978
Qy 841 CCCGAGCGCATGCGCTTCATCCGCTCCGCGTATCCGTTCCGCGGAGAGGCGT 900
Db 979 CCCGAGCGCATGCGCTTCATTCATGAGATGATCCATTCCTACAGAGAGAGGCGT 1038
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Db 1099 CTTCGCGCGCTC 1110

RESULT 4

US-09-791-138A-3/c
; Sequence 3, Application US/09791138A
; Publication No. US20040106178A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jun
; APPLICANT: Ackerman, Eric
; TITLE OF INVENTION: Proteins in a Porous Support
; FILE REFERENCE: E-1741
; CURRENT APPLICATION NUMBER: US/09/791,138A
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 3
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: The organism is unknown per ATCC (#67778)
US-09-791-138A-3

Query Match 63.6%; Score 624.6; DB 11; Length 1029;
Best Local Similarity 77.5%; Pred. No. 1e-130;
Matches 756; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

Qy 2 GCGCGATCATCTTCGAGGCGCGCTTACCTTCACCCAGACGACATCTGCGGCTTC 61
Db 977 GGTCTATCAACATCTGAGAGCGGCTTTCACACTGATCTCAAGACACATCTGCGGAC 918

QY 62 TCCGCGGCTTCTCCGCGCTGAGCGAGTTCTTCCGCTCCCGAAGGCTCCGCGAG 121
 Db 917 TCGGAGGATTCCTGCTGCTTGGCCAGAGTTCTTCCGAGCGGAAAGCTCTACCGGAA 858
 QY 122 AAGGCGGCGGCGGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 181
 Db 857 AAGGCTGTGAGAGGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 798
 QY 182 TCCACCTTCGACATGCG 241
 Db 797 TCGACTTCGATATCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 738
 QY 242 GTGCACTGTGAGCG 301
 Db 737 GTTCATATCGTGGCG 678
 QY 302 TCCGCGGAGAGCTCAACCACTTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 361
 Db 677 AGGTGAGAGGAACTCACAGATTCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 618
 QY 362 GGCATCCG 421
 Db 617 GGAATTAGGCG 558
 QY 422 CTCGTCTCAAGCG 481
 Db 557 TTAGTGTAAAGCG 498
 QY 482 ACCGCGCGCTCCGAGCG 541
 Db 497 ACGGAGAGAGTCAAGCGAGTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 438
 QY 542 TCCCGCTCCG 601
 Db 437 AGCCCTCAACGGGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 378
 QY 602 GCCCTCG 661
 Db 377 GCCCTCG 318
 QY 662 CTCGAGGAGCAAGCG 721
 Db 317 CTAGAGATTAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 258
 QY 722 CTCCTCATCAAGCG 781
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 QY 782 TGGCTCTTGGGCTTCT 841
 Db 197 TGGCTCTTGGGCTTCT 138
 QY 842 CCGGAGCGGATGCG 901
 Db 137 CCGGAGCGGATGCG 78
 QY 902 CCGGAGAGAGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 961
 Db 77 CCAAGAGGAAAGCG 18
 QY 962 CTCGCGCGCT 976
 Db 17 TTGCGGCGCGCTCATGA 3

RESULT 5
 US-10-477-469-6
 ; Sequence 6, Application US/10477469
 ; Publication No. US20040161818A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horne, Irene
 ; APPLICANT: Sutherland, Tara

; APPLICANT: Harcourt, Rebecca
 ; APPLICANT: Russell, Robyn
 ; APPLICANT: Oakeshott, John
 ; TITLE OF INVENTION: Phosphotriesterase from Agrobacterium radiobacter P230
 ; FILE REFERENCE: 131-03
 ; CURRENT APPLICATION NUMBER: US/10/477,469
 ; PRIOR FILING DATE: 2003-11-12
 ; PRIOR APPLICATION NUMBER: PCT/AU02/000594
 ; PRIOR FILING DATE: 2002-05-15
 ; PRIOR APPLICATION NUMBER: AU PR 5023
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 1071
 ; TYPE: DNA
 ; ORGANISM: Agrobacterium radiobacter
 US-10-477-469-6
 Query Match 57.7%; Score 566.8; DB 18; Length 1071;
 Best Local Similarity 74.0%; Pred. No. 8.8e-118;
 Matches 718; Conservative 0; Mismatches 252; Indels 0; Gaps 0;
 QY 1 CGGCGCGATCAACATCTCCGAGCGCGCGCTTACCTTCAACCGAGCAATCTGGGCTC 60
 Db 36 CGGCGCGATTCAGATTTCGAGAGGCGGCTTCACATGACCATGAGCATATCTGGGCG 95
 QY 61 CTCGCGCGCTTCCG 120
 Db 96 TTCGCGGAGATTCTTACGTGCGGTGCGGAGTTTGTGATGCGCGAAGCTTACGCG 155
 QY 121 GAAGCGGTGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
 Db 156 AAGGCTGTGAGAGATTAGCGCATGCGAGATCGGCTGGGTGAAACATCGTGAATG 215
 QY 181 GTCACTTTCAGATTCG 240
 Db 216 GTCACTTTCAGATTCG 275
 QY 241 CGTCAATCGTGGCG 300
 Db 276 GTTCAATCGTGGCG 335
 QY 301 CTCGTGAGAGGATCTACCCAGTTCTTCTCCGAGATTCAGTCAAGCGATCGAGCAC 360
 Db 336 CAGGTCGAGAGATGAGCCAGTTCTTCTGCGGAAATCAACATGAGATCGAAGCAC 395
 QY 361 CGGATCCG 420
 Db 396 CGGATTAAGGCG 455
 QY 421 GCTGTGTCAAGGCG 480
 Db 456 GTTGTGTAAAGGCG 515
 QY 481 CAGCGCGCTCCCGAGCG 540
 Db 516 CAGGTCAAGAGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 575
 QY 541 CTCCTCCG 600
 Db 576 GAGCCCTCAAGGCTTGTATCGGTCAAGGAGATGATGATGATGATGATGATGATG 635
 QY 601 CGGCTCG 660
 Db 636 CGGCTCG 695
 QY 661 CTTGAGAGCAACGCTTCG 720
 Db 696 TCTGAGAGCAATCGAGTGAATTAAGCGCTTGTGATCTCGGCGGTGCGAAGAGGCG 755
 QY 721 CTTCTATCAAGGCGCTTATCGACAGGCGTACATAGAGATCTCTGTGTCAAGCA 780

Db 756 TCTCTTGATCAAGCGCTCATCGACCGAGCTAACAGAGTCAATCTCTGCTCCCATGA 815
Qy 781 CTGGCTCTTCGGGCTTCTCTCTTAAGTACCAATCATGAGACGATGAGACCGCGTAA 840
Db 816 CTGGCTCTTCGGGCTTCTCTCTTAAGTACCAATCATGAGACGATGAGACCGCATAAA 875
Qy 841 CCCGACGCGATGCGCTTTCATCCCGCTCCGCTGATGCCGCTCTCTCCGAGAAAGGCGT 900
Db 876 CCCAGATGGAATGCGCTTCTCTCTTAAGTACCAATCATGAGACGATGAGACCGCGT 935
Qy 901 GCCGACGAGACCTTCGCGCGGATACCGTGAACCAACCGCGCGCTCTCTCCCGAC 960
Db 936 CCCGCGGAGAAACGCTGACGAGGCTAACCGTGGCCAAATCCGCGGCTTCTGTCAACGAC 995
Qy 961 CCTCGCGGCC 970
Db 996 CTGCGGCGCC 1005

RESULT 6

US-10-477-469-5
; Sequence 5, Application US/10477469
; Publication No. US20040161818A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Irene
; APPLICANT: Sutherland, Tara
; APPLICANT: Harcourt, Rebecca
; APPLICANT: Russell, Robyn
; APPLICANT: Oakeshott, John
; TITLE OF INVENTION: Phosphotriesterase from *Agrobacterium radiobacter* P230
; FILE REFERENCE: 131-03
; CURRENT APPLICATION NUMBER: US/10/477,469
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/AU02/000594
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: AU PR 5023
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: *Agrobacterium radiobacter*
US-10-477-469-5

Query Match 57.7%; Score 566.8; DB 18; Length 1155;

Best Local Similarity 74.0%; Pred. No. 8.8e-118;

Matches 718; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

Qy 1 CGGCCGATCAATCTCCGAGCGCGCTTCACTCCACCCGACGACATCTGGGCTC 60
Db 120 CGGCCCATTTCCAGTTTGGAGCGGCTTCACTGACCCATGACATATCTGGGCGAG 179
Qy 61 CTCGCGCGGCTTCTCCGCGCGCTGCGCGAGTTCTTTCGCGCTCCGCAAGGCCCTTCGCCGA 120
Db 180 TTCGCGGAGATTCCTACGAGGTGGCGGAGTTTTCGTAACCGCAAGCTCTAGCGGA 239
Qy 121 GAAGGCGTGGCGCGCTCCG 180
Db 240 AAAGGCTGTGAGAGGATTAACGACATGCGAGATCGGCTGCGCAAAACATCTGTGATGT 299
Qy 181 GTCCACTTTCGACATCGCGCGCGCGAGTGTCCCTCTCGCGCGAGTGTCCCGCGCGCGCGGA 240
Db 300 GTCCACTTTCGACATCGCGCGCGCGAGTGTCCCTCTCGCGCGAGTGTCCCGCGCGCGCGGA 359
Qy 241 CGTGACATCTGTGCGCGCGCGCGCGCTGTGTGACCCCGCGCTCTCCATGCGCGCTCG 300
Db 360 CGTGATATCTGTGCGCGCGCGCGCGCTGTGTGACCCCGCGCTCTCCATGCGCGCTCG 419
Qy 301 CTCGCTGAGAGACCTCCAGGTTCTCTCTCGCGAGATCCGATACGAGATGAGAGAC 360
Db 420 CAGCGTCAAGAGACCTCCAGGTTCTCTCTCGCGAGATCCGATACGAGATGAGAGAC 479

Qy 361 CGGACCTCGCGCGCGCATCATCAAGTGGCCACACCGGACAGCCGCCGTTCCAGGA 420
Db 480 CGGATTAAGGCGGCGCATTAATCAAGTGGCCACACCGGAGAGGCGACCCCTTTCAAGA 539
Qy 421 GCTGTGCTCAAGGCGCGCGCGCGCTCTCTCGCGACCGGCGTGGCGTGAACCA 480
Db 540 GTTGTGTTAAAGGCG 599
Qy 481 CACGCGCGCTCCGAGGCG 540
Db 600 CACGTCAAGCATGACG 659
Qy 541 CTCGCGCGTCCGCGTGTGATCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 660 GAGCGCGTCAAGGCG 719
Qy 601 CGCGCTCG 660
Db 720 CGGCTCGCTCG 779
Qy 661 CCTGAGAGCAACGCGCTCCG 720
Db 780 TCTGAGAGCAATGAGCGATTAAGCGCTTTGATCTCGGTGTGGCAAAACAGGCG 839
Qy 721 CCTCTCATCAAGGCG 780
Db 840 TCTCTGATCAAGGCG 899
Qy 781 CTGGCTCTTCGGGCTTCTCTCTTAAGTACCAATCATGAGACGATGAGACCGCGTAA 840
Db 900 CTGGCTCTTCGGGCTTCTCTCTTAAGTACCAATCATGAGACGATGAGATGCGATAAA 959
Qy 841 CCCGACGCGATGCGCTTTCATCCCGCTCCGCTGATCCGCTCTCCGCGAGAGGCGGT 900
Db 960 CCCAGATGAATGCGCTTCTCTCTTAAGTACCAATCATGAGACGATGAGATGCGATAAA 1019
Qy 901 GCCGACGAGACCTTCG 960
Db 1020 CCCGCGGAGAAACGCTGACGAGGCTAACCGTGGCCAAATCCGCGGCGTTCTGTACGAC 1079
Qy 961 CCTCGCGGCC 970
Db 1080 CTGCGGCGCC 1089

RESULT 7

US-10-477-469-8

; Sequence 8, Application US/10477469

; Publication No. US20040161818A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Irene

; APPLICANT: Sutherland, Tara

; APPLICANT: Harcourt, Rebecca

; APPLICANT: Russell, Robyn

; APPLICANT: Oakeshott, John

; TITLE OF INVENTION: Phosphotriesterase from *Agrobacterium radiobacter* P230

; FILE REFERENCE: 131-03

; CURRENT APPLICATION NUMBER: US/10/477,469

; PRIOR FILING DATE: 2003-11-12

; PRIOR APPLICATION NUMBER: PCT/AU02/000594

; PRIOR FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: AU PR 5023

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 1155

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: Mutant of Opda

; OTHER INFORMATION: Mutant of Opda

US-10-477-469-8

Query Match 57.6%; Score 565.2; DB 18; Length 1155;
Best Local Similarity 73.9%; Pred. No. 2e-117;
Matches 717; Conservative 0; Mismatches 253; Indels 0; Gaps 0;

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1 CGGCGCATCAACATCTCCGAGCGCGGCTTCAACCTCCACCCCAAGGCAATCTGCGGCTC 60
Db CGGCGCATCAACATCTCCGAGCGCGGCTTCAACCTCCACCCCAAGGCAATCTGCGGCTC 179
Qy 61 CTCGCGCGGCTTCTCCGCGCGCTTCCGAGTTCTTCGAGCTCCCGCAAGGCGCTTCGCGA 120
Db TTCGCGCGGAGTTCTTACGAGCGGTGCGCGAGTTTTCGGTAGCGCAAGCTCTAGCGGA 239
Qy 121 GAAGCGCGTGGCGGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db AAAAGCTGTGAGAGGATTACGCAATGCGCAAGATCGCTGCGCGCAAAACATCTGCGAGT 299
Qy 181 GTCCACCTTCGACATCGCGCGCGAGGTGCTCCCTCCGCGCGAGGTGCTCCGCGCGCGCG 240
Db GTCCACCTTCGATTCGAGTCTGAGCTCCGCTTATTTGCGCGAAGTTTCCGCGCGCGCG 359
Qy 241 CGTGACATCTGCGCGCGCGCGCGCGCTGCTGCTGCGCGCGCGCGCTCTCCATGCGCGCTCG 300
Db CGTGACATCTGCGCGCGCGCGCGCGCTGCTGCTGCGCGCGCGCGCTCTCCATGCGCGCTCG 419
Qy 301 CTCGCGGAGAGCTCACCCAGTTCTTCTCCGCAATCCAGTACGCGATCGAGACAC 360
Db CAGCCTCCAGAGAACGACCCAGTTCTTCTCGGTGAAATCCAAATGCGCATGGAAGACAC 479
Qy 361 CGGCAATCGCGCGCGCGCATCATCAAGTGGCCACCGCGCAAGGCGCGCGCGCGCGCGCG 420
Db CGGATTTAGGCGCGCGCATTTATCAAGTGGCCACCGCGCAAGGCGCGCGCGCGCGCGCG 539
Qy 421 GCTCGTGTCAAGCGCGCGCGCGCGCGCTCCCTCCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Db GTTGATTTAAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 599
Qy 481 CACCGCGCGCTTCCAGCGCGAGCGAGGAGGAGGCGCGCGCGCGCATTTTGAATCGGAGGCT 540
Db CACGTCACAGATCAGCGCGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659
Qy 541 CTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
Qy 601 CGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 779
Qy 661 CTTGAGAGACACGCTCCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db TCTAGAGGCAATGAGATGCAATGAGCGCTCTTGTGTCTCGGTGTGCGCAAAACAGGCG 839
Qy 721 CTTCTCATCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db TCTCTTGAATCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 899
Qy 781 CTGCGCTTTCGCGCGCTTCTCTCTCAAGTACCAATCATGAGCGTGAAGCGCGCGCG 840
Db CTGCGCTTTCGCGCGCTTTCGAGCTATGTCAAGAACATCATGAGCGTGAAGCGCGCG 959
Qy 841 CCGCGAGCGCATGCGCTTCTCATCTCCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db CCGAGATGGAATGCGCTTCTCTCTCAAGTATCCCATTTCTTCAAGAGAGAGGCGGT 1019
Qy 901 GCGCGAGGAGACCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db CCGCGAGGAGAGCGCTTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1079
Qy 961 CTTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 970
Db CTTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1089
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RESULT 8
US-10-477-469-7
; Sequence 7, Application US/10477469
; Publication No. US20040161818A1
; GENERAL INFORMATION:
; APPLICANT: Home, Irene
; APPLICANT: Sutherland, Tara
; APPLICANT: Harcourt, Rebecca
; APPLICANT: Russell, Robyn
; APPLICANT: Oakeshott, John
; TITLE OF INVENTION: Phosphodiesterase from Agrobacterium radiobacter P230
; FILE REFERENCE: 131-03
; CURRENT APPLICATION NUMBER: US/10/477,469
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/AU02/000594
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: AU PR 5023
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant of Opda
US-10-477-469-7

Query Match 57.2%; Score 562; DB 18; Length 1155;
Best Local Similarity 73.7%; Pred. No. 1e-116;
Matches 715; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

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1 CGGCGCATCAACATCTCCGAGCGCGGCTTCAACCTCCACCCCAAGGCAATCTGCGGCTC 60
Db CGGCGCATCAACATCTCCGAGCGCGGCTTCAACCTCCACCCCAAGGCAATCTGCGGCTC 179
Qy 61 CTCGCGCGGCTTCTCCGCGCGCTTCCGAGTTCTTCGAGCTCCCGCAAGGCGCTTCGCGA 120
Db TTCGCGCGGAGTTCTTACGAGCGGTGCGCGAGTTTTCGGTAGCGCAAGCTCTAGCGGA 239
Qy 121 GAAGCGCGTGGCGGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db AAAAGCTGTGAGAGGATTACGCAATGCGCAAGTGGCGCGCGCGCGCGCGCGCGCGCG 299
Qy 181 GTCCACCTTCGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db CGGATTTAGGCGCGCGCATTTATCAAGTGGCCACCGCGCAAGGCGCGCGCGCGCGCG 359
Qy 241 CTTGAGAGACGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db TCTAGAGGCAATGAGATGCAATGAGCGCTCTTGTGTCTCGGTGTGCGCAAAACAGGCG 419
Qy 301 CTCGCGGAGAGTCAACCGAGTTCTTCTCCGCGAGATCCAGTACGCGATCGAGACAC 360
Db CAGGCTGGAAGAACGACCCAGTTCTTCTCGCGAGAAATCCAAATGCGCATGGAAGACAC 479
Qy 421 CCGCGATCGCGCGCGCGCATCATCAAGTGGCCACCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db CCGATTTAGGCGCGCGCATTTATCAAGTGTCTGCAACAGAGGAGCGCGCGCGCGCGCG 539
Qy 480 CGGATTTAGGCGCGCGCATTTATCAAGTGTCTGCAACAGAGGAGGAGGAGGAGGAGG 540
Db CCGATTTAGGCGCGCGCATTTATCAAGTGTCTGCAACAGAGGAGGAGGAGGAGGAGG 659
Qy 481 CACCGCGCGCTTCCAGGCGCGAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
Db CAGGTCAGCAAGTACGCGCGAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659
Qy 541 CTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
Qy 601 CGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
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Db      720  CGGCTCGCTGCGCGCGGATACCTGCTGTTAGATGACGCTACGATGCGATTGG 779
Qy      661  CCTGAGAGCAACGCTCCGCGTCCGCTCTCTGCGGATCCGCTCTCTGAGAACCGCGC 720
Db      780  TCTGAAAGGCAATCGAGTGAATTAGCGCTCTTGGTCTCGCTGCTGGAACAAAGGCG 839
Qy      721  CCTCTCATCAAGGCGCTCATGACGAGGCTACATGAAGAGATCCTGCTCAAGCA 780
Db      840  TCTTTGATCAAGGCGCTCATGACGAGGCTACATGAAGATGAAATCTCTCTCCATGA 899
Qy      781  CTGCTCTTCCGCTTCTCTCTCTACGTGACCAACATGACGATGACGCGGTGA 840
Db      900  CTGGCTGTTGGGTTTTCGAGCTATGTCAGAAACATGACGTAAATGCAATGCAATAA 959
Qy      841  CCGGACGCGCATGCGCTTCTCATCCGCTCCGCTGATGATGCTCTCTCTGAGAAAGGCGT 900
Db      960  CCGAGATGGAATGGCGCTTCTCTCTCTGAGATGATCCATCTCTCAAGAGAAAGGCGT 1019
Qy      901  GCGGAGAGAGACCTCGCGCGCATGACGCTGACCAACCGCGCGCTTCTCTCTCCGAGC 960
Db      1020  CCGCGGAGAAACCTAGACAGGCGTAAACGCTGCGCAATCCGCGGCTTCTCTCTCACCGAC 1079
Qy      961  CCTCGCGCGC 970
Db      1080  CGTGGCGCC 1089

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RESULT 9 US-10-282-122A-25658

; Sequence 25658, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25658

; LENGTH: 978
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25658

Query Match 17.0%; Score 167.4; DB 17; Length 978;
Best Local Similarity 51.2%; Pred. No. 2.3e-28;
Matches 467; Conservative 0; Mismatches 416; Indels 30; Gaps 2;

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Qy      1  CGGCCCCATCAACATCTCCGAGCGCGCTTACCCCTACCCAGAGACATCTGCGGCTC 60
Db      24  CGGCCCCATCAACATCTCCGAGCGCGCTTACCCCTACCCAGAGACATCTGCGGCTC 83
Qy      61  CTGCGCGGCTTCTCTCCGCGCTTCTGAGGATCTTCTGCTCTCCGAGAGCCCTGCGCA 120
Db      84  GACCAACGAGATCCGAGAAATACCCGAGAGGATGAGGAGAGAGAGAGAGAGAGAGAG 143
Qy      121  GAGGCGCTGCGCGGCTTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 180
Db      144  CGAGCGCATGACCGGCTCAACGAGCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 203
Qy      181  GTCCACCTTGACATCCGCGCGCGAGAGTCTCTCTCTGCGAGGAGTCCGCGCGCGCGCA 240
Db      204  CACGTCATCGGCGCTGCGCGCTGCTACATTCGCGCATGCGCGGATCGCGCGCGCGCA 263
Qy      241  CGTGCAATCGTGGCGCGCGCGCGCGCTGCTGAGACCGCGCGCTTCTCATGCGGCTCG 300
Db      264  GCTGAATATCTGTGTGGGAAAGGGGCTTTACACCTGACAGAGATGCGCTTATTTCA 323
Qy      301  CTCGCT-----GAGAGCTCACCCAGTTCTTCTCTCG 333
Db      324  CTACCTGGGCGCGGCGCGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCG 383
Qy      334  CGAATTCAGTACCGGATACGAGACACCGGATCCGCGCGCGCGCGCGCGCGCGCGCGAC 393
Db      384  CGAATTCAGGAGGCGATCGCGGACCGGATCAAGCGCGCGCGCGCGCGCGCGCGCGCGAC 443
Qy      394  ---CACGGCAAGGCAACCCGCTTCAGAGAGCTGCTGCTCAAGGCGCGCGCGCGCGCTC 450
Db      444  TGAGCACCAGCGCTGCTGCTGCGGCGGCTGAGAGGCTGCGGCGCGCGCGCGCGCGCG 503
Qy      451  CCTCGCACCGGCGGCTGCGGATGACCAACCGCGCGCGCTTCCAGCGCGAGCGAGCA 510
Db      504  CAAGCGCACCGGCGGCTGCGGATGCTCCAGCACCAACCGCGCGCGCGCGCGCGCGCTCG 563
Qy      511  GAGGCGCGCATCTTCTGAGTCCGAGGCGCTTCCCGCTCCCGCGCTGATGCGGCACTC 570
Db      564  CGAGCGCGGATCTTCTGAGGAGGCGGCTGCACTGAGCGCGGATGATGCGGCGCTTC 623
Qy      571  CGAGGACCGAGCGACTCTCTTACCTTACCGCGCGCGCGCGCGCGCGCGCGCGCTAC 630
Db      624  CGGCGACGAGCGAGCTGCTGCTTACCTGAGAGGCTTACCTGCGCGCGCGCGCTTAC 683
Qy      631  CCTCGACCAATCCCGCATCTCGGATCGGCTGAGAGCAAGCGCTCGCGCGCTCGCGCT 690
Db      684  CATGACCGGATTCGAGATGAGCGATCTCGCGCTTACGAGCGCGGATGAGCATGCTCGC 743
Qy      691  CTTGCGCATCCGCTCTTGGCAAGACCGCGCGCTTCTCATCAAGGCGCTTATGAGCAAG 750
Db      744  GCGATGTCGAGCGCGCGCGCGCGAGCAAGATGCTGCTGCGAGCGCGCGCGCGCGCT 803
Qy      751  CTACATGAAGAGATCTCTGTCACAGCACTGCGCTTTCGCGCTTCTCTCTTACGTCAC 810
Db      804  TTTTCAGCGACTTCCCGAGAGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 863
Qy      811  CAACATCAATGAGCGTATGAGCGCGGTGACCGCGAGCGCGCGCGCGCGCGCGCGCTCG 870
Db      864  CATTCACAGAGCGTATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 923
Qy      871  CGTATCCCGCTTC 883
Db      924  CACCATGCTGCTC 936

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RESULT 10
US-10-282-122A-28172
; Sequence 28172, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 28172
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28172

Query Match      16.9%; Score 166.4; DB 17; Length 981;
Best Local Similarity 55.5%; Pred. No. 3.8e-28;
Matches 382; Conservative 0; Mismatches 276; Indels 30; Gaps 2;
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QY 1 CGGCCCCATCACATCTCTCCGAGCGCGGCTTCACTCCACCGACGACATCTGGGCTC 60
DB 24 CGGACCCATTCACACCGCTGATCTCGGCGTACGCTGATGACGACGACGCTTCATCAT 83
QY 61 CTCGCGCGGCTTCTCTCGGCGCGTGGCGGAGTCTTTCGCGCTCCCGCAAGGCGCTGCCGA 120
DB 84 GACCAACGAGATGGCGGAGAACTACCGGAGCGCTGGGAGCGAGACGAGCAAGCGGCTGAC 143
QY 121 GAAGCGCGTGGCGGCTCTCG 180
DB 144 CGGCGCGCATCGCGCGCGCTAGGAGAACTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 203
QY 181 GTTCACTTTCGACATCG 240
DB 204 CACGCTGATCGGCG 263
QY 241 CGTGCACATCGTGGCGCGCGCGCGCGCGCTGCTGTGACCGCGCGCTCTCAATGCGCTCG 300

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DB 264 GCTGACATCGTCTGTGGCCACCGGCTGTACACCTACACGATCCCGTTCTACTTCCA 323  
QY 301 CTCGCT-----GGAGAGCTCACCCAGTTCTTCTCTCG 333  
DB 324 CTACCTCGGGCGGGCGGACAGCTGACCGCGCGGAGATCATGACCGACATGTTGTCTCG 383  
QY 334 CGAGATTCAGTACCGCATCGAGACATCGGCAATCCGCGCGCGCATCATCAAGTGGCCAC 393  
DB 384 CGACATTCAGACGCGCATCGCGACACCGGCATCAAGCGCGGAAATCTTCAAGTGGCCAC 443  
QY 394 CACCGGCAAGGC---CACCGGTTCCAGGAGCTGTGCTCAAGGCGCGCGCGCGCTC 450  
DB 444 CGACGACCGGCGCTCACCCCTTGCTGTGACCGGCTGTGGCGCGCTGCTTCAAGCA 503  
QY 451 CTCGCGCACCGCGCGTGGCGGTGACCAACCAACCGCGCGCTCCGACCGCGAGCGAGCA 510  
DB 504 CAAGCGCACCGGCGGCGCGATCTCACCAACCAACCGCGCGCGGCGCGCGCGCTTGA 563  
QY 511 CGAGCGCGCATCTTTCGAGTCCGAGGCGCTTCCCGCTCCGCGGTGTGATCGGCACTC 570  
DB 564 CCAGCAACGCACTTTCGCGCGAGAGGCGGTGACCTGAGCGGCTGTATCGACACTG 623  
QY 571 CGAGCACCGGACGACCTCTCTCACTGACCGCGCGCGCGCGCTACCTCATCG 630  
DB 624 CGGCGACGACACGACGCTGCTGCTTCTGGAAGACTCATCGCGCGGCTCTTACTTGG 683  
QY 631 CCTGACCACTCCGCGCACTCGGCATC 658  
DB 684 GATGACCGGTTTCGCGCGTGCAGCTGATC 711
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RESULT 11
US-10-282-122A-26226
; Sequence 26226, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 26226
LENGTH: 918
TYPE: DNA
ORGANISM: Mycobacterium bovis
US-10-282-122A-26226

Query Match 15.2%; Score 148.8; DB 17; Length 918;
Best Local Similarity 54.9%; Pred. No. 3.3e-24;
Matches 356; Conservative 0; Mismatches 262; Indels 30; Gaps 2;

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QY 41 CACGAGCAATCTGCGGCTCTCCGCGGCTTCTCCGCGGAGTTCTTCGCG 100
DB 4 CACGAGCAATCTTATATGACCAACGATTGGGCAAGACTACCCGAAACCTGGGCG 63
QY 101 TCCCGCAAGCCCTGCGGAGAAAGCCGTGCGGCGCTCCGCGCGCGCGCGCG 160
DB 64 GACGAGGACAAAGCGGCTGCGCGGCACTGCGCGCTAGCGAACTCAAGGCGCGCG 123
QY 161 GTCGCGACATGCTGGAAGCTGTCACCTTGAATCGGCGGAGAGTGTCTCTCGCG 220
DB 124 GTGAGACCATGTGACCTCAAGGTGATCGGAGTGGGCGGATACCTCCGCGCATGCG 183
QY 221 GAGGTGTCGCGCGCGCGCGAGCTGCAATGCTGCGCGCGCGCGCTGTGTTGACCG 280
DB 184 CGGCTGCGCGCGCGCGCGAGCTGAACATGCTGTGCGCGCGCGCTGTGTTGACCTG 243
QY 281 CGGCTGCTCAATGCGCGCTCGGCTCGT-----GGAGAG 313
DB 244 GACGTCCGCTTCTACTTCCACTACCTCGGCGCGCGCGCGAGCTGAGCGCGGAGATC 303
QY 314 CTCACCGAGTTCTTCTCCGCGAGATTCAGTACGGATGAGAGACACCGCGATCCGCG 373
DB 304 ATGACCGAGATGTGTGTCGCGCAATCGAGCAAGCATGCGCGACCTCGCATCAAGGG 363
QY 374 GGCATCATCAAGTGGCGCAACCGGCAAGC---CACCCGTTCCAGAGCTGTGCTC 430
DB 364 GGAATCTCAATGCGCGCAACCGGCGCTACCCCTGTGCTGAGGCGGCTGTTG 423
QY 431 AAGCGCGCGCGCGCGCTCTCCGCGACCGCGGTGCGGTGACCAACCGCGCGCG 490
DB 424 CGCGCGGTGCGCGCAAGCAACGCAACCGCGCGCGCGCTCCACCCACCGCGCG 483
QY 491 TCCCAAGCGGAGGAGGAGCGCGCGCATCTTGAATCGGAGGCGCTCTCCCGTCC 550
DB 484 GGGCTGCGCGCGCGCTTGACCAAGCAACGATCTTCCGAGAGAGGGGTGAACCTGAG 543
QY 551 CGCGGTGATCGCGCACTCCGAGCAACCGAGCACTCTCTTACCTCAACCGCGCTGCG 610
DB 544 CGGCTGTTATGAGACCTGCGCGGCAAGCACTGAGCTGCGCTACTTGAAGAAGCTCAT 603
QY 611 GCCCGCGGCTCATCTGAGCTCGACCAATCCGCGACTCCGCGATC 658
DB 604 GCCCGCGGCTCTACTCGGATGAGCGGCTGCGCGCTGAGCTGATC 651
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RESULT 12
US-10-363-31407/c

Sequence 31407, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
NUMBER OF SEQ ID NOS: 2003-03-03
SEQUENCE OF SEQ ID NOS: 40712
LENGTH: 985

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
US-10-363-31407

Query Match 13.9%; Score 136.2; DB 18; Length 985;
Best Local Similarity 47.9%; Pred. No. 2.2e-21;
Matches 428; Conservative 0; Mismatches 458; Indels 7; Gaps 1;

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QY 1 CGGCCGATTCACATCTCCGAGCGCGGCTTCACTCCACCAAGACATCTGCGCTC 60
DB 984 CGTCAACATTCACATCTACATCTACATCTACATCTACATCTACATCTACATCTAC 925
QY 61 CTCGCGCGCTTCTCCGCGCTGCGCGGAGTTCTTCCGCTCCGCGAGCCCTGCGCA 120
DB 924 CATCTAGCTGACATCTAGCTGACCTGACATCTAGCTGACATCTAGCTGACATCTA 865
QY 121 GAAAGCGGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 864 CGTCAACATTCACATCTACATCTACATCTACATCTACATCTACATCTACATCTA 805
QY 181 GTTCACTTCAATCGGCGCGCGCGGCTGCTCTCTCGCGAGGTGTCGCGCGCGCA 240
DB 804 CCGTCAAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTG 745
QY 241 CGTCAAC-----TCGTGCGCGCGCGCGCGCTGCTGCTGCTGCAACCGCGCTTCGATGC 293
DB 744 CATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTG 685
QY 294 GCTTCGCTCGTGGAGAGGCTCAACCGGCTTCTCTCCGAGATTCAGTACGCGATGC 353
DB 684 ACATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTG 625
QY 354 AGGACCGGCGCTCCGCGCGCGCGCATCAAGTGGCGCAACCGGCAAGCGCGCGCT 413
DB 624 AGTCAAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTG 565
QY 414 TCCAGAGCTGCTCAAGGCGCGCGCGCGCTCTCTCTCGCGCGCGCGCGCTG 473
DB 564 ACATGAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTG 505
QY 474 CCACCGACCGCGCGCTCCGCGCGCGCGCGGAGGAGGAGCGCGCGCATCTTGAAGTCC 533
DB 504 AGCTTACATCAACATCAACATCTACATCTACATCTACATCTACATCTACATCTA 445
QY 534 AGGCGCTTCCCGCGCGCGCGGTGATCGGCGCATCTCCGAGCAACCGAGCACTCTCT 593
DB 444 ACATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTAGCTG 385
QY 594 ACCTACCGCGCTCCGCGCGCGCGGCTACTGCTGAGCTGAGCAACATCCGCGACTCC 653
DB 384 AGCTGAGATCTACCTGACATCTAGCTGACATCTAGCTGACATCTAGCTGACATCTA 325
QY 654 CCATGCGCTGAGAGCAACGCTCCGCGCGCGCGCTCTCTCGCGCATCCGCTCTGCGAGA 713
DB 324 ACATCTAGCTCAACGCTTACATCTAGCTGACATCTAGCTGACATCTAGCTGACAT 265
QY 714 CCGCGCGCTCTCTCAAGGCGCTCAAGCGGCTACAGGCTACATGAGAGCACTCTGCT 773
DB 264 AGCTGAGATCTAGCTCAACGCTGAGCTGAGCTGAGCAACATGAGCACTGAGCACT 205
QY 774 CCAAGACTGCTGCTTCCGCTTCTCTCTCTGAGTACCAACATGAGAGTGAAGTGA 833
DB 204 AGCTGAGATCTAGCTCAACGCTGAGCTGAGCTGAGCAACATGAGCACTGAGCTG 145
QY 834 GGTGAACCGGAGGAGGAGGCTTCACTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 886
DB 144 ACATCTAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 92
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RESULT 13

484 | GCGCGCTCCAGCGCGAGCGAGAGGAGCGCGCATCTTGAGTCCGAGGGCCCTTC 543
Db | CCGCATCCGCATCCGCATCGCGATCGCGCATCCGCATTCGATCGCGTCAAGATCCGCAT 607
Qy | CCGGTCGCGCGTGTGCATCGGCACTCCGACGACACCAGACACTCTCTACTACCGC 603
Db | CCGCGTCAGCATCAGCATCCGCATCGCGCTCAGCATCCGCATCCGCATCCGCATCGCAT 547
Qy | CCTCGCCGCCCGCGGCTACCTCATCGGCTCCGACCACTCCGCACTCCGCGATCGGCT 663
Db | CTGCATCGGCGTACGATGAGCATCCGCGTCGCGATCAGATCCGATCCGATTCGATCGGCAT 487
Qy | CGAGACAAACGCTCCGCGCTCCGCTCTCTCGGCATCCGCTCTCGACAGACCCGCGCT 723
Db | CGCATCCGCATCTGCATCGGCGTCAAGCATCCGCGTCAAGGTGGCATCAGATCCGCAT 427
Qy | CCTATCAAGGCGCTCATCGACCAAGGCTACATGAAGCAATCTCTGTCTCAACGATG 783
Db | CGGCTTCAGCATCCGCATCGGCGTCAAGATCCGCATCCGCATCGGCGTCAAGCTCAGCAT 367
Qy | GCTCTTCGCGCTCTCTCTCTACGTGACCAATCATGACGATGACCGCGCTGAACC 843
Db | CGGCATCCGCATCCGCATCGGCGTCAAGGTCAAGCTCAGCATCCGCATCCGCATCGCGCTCAGCAT 307
Qy | GAGCGGCATGCGCTTCATCCCGCTCCGCT---GATCCGTTCTCCGCGAGAAGGCGT 900
Db | CGGCGCTCGGCATCCGCATCCGCATCAGCGTCAAGCATCCGCATCGGCGTCCGCTTCGCGT 247
Qy | GCCGAGAGAGACCTTCGCGGCGATCAACGTCAGCAACCCGCGCTCTCTCTCCCGAC 966
Db | CGGCGTCAGCATCCGCATCCGCATCGGCGCTCGGCATCCGCATCCGCATCCGCAT 187
Qy | 961 C 961
Db | 186 C 186

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RESULT 15
US-10-398-221-613
; Sequence 613, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederick
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 613
; LENGTH: 1311
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-613

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Query Match	12.5%	Score 122.6;	DB 17;	Length 1311;
Best Local Similarity	46.2%;	Pred. No. 2.4e-18;		
Matches 444;	Conservative 0;	Mismatches 514;	Indels 3;	Gaps 1

QY 4 CCGCATTCACATTCCTCCGAGGCGGGCTTACACCTTCACCCAGACACATCTGGGGCTCTTC 63
Db 190 CCGCATCTGCATTCGGATATCCGATCAGGCTCAGACATCCGCATAGGCTGGGGCTCAGGCTCGGCAT 249
QY 64 CGCCGGGCTTCTCTCCGGCGCTGCGCCGGAATTTCTTGGGCTCCCGCAGGCGCCTCGCCGAGAA 123
Db 250 CTGCATTCGGCATCTGCATCGGCATCAGCGTGGCGGTAGGATCCGATCCGATCAGCGCTGGGCAT 309
QY 124 GGCCTGTGCGGCGCTTCGCGCGCGCGCGCGCGCGCGCGGTGCGGACCATCTGTGACGTGTC 183

[illegible]

Search completed: February 12, 2005, 06:40:04
Job time : 478 secs

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241 CGTGCACATCGTGGCCGACCGGCTCTGGTTGACCCCGGCTCTCCATGCGCTCCG 300
242 CGTGCACATCGTGGCCGACCGGCTCTGGTTGACCCCGGCTCTCCATGCGCTCCG 400
301 CTCGGTAGAGAGCTCACCAGTTCTTCTCCGCGAGATCCAGTACCGGATCGAGAGAC 360
401 CTCCTGAGAGAGCTCACCAGTTCTTCTCCGCGAGATCCAGTACCGGATCGAGAGAC 460
361 CGGCATCCGCGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAGG 420
461 CGGCATCCGCGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAGG 520
421 GCTGCTCTCAAGGCGCGCGGCTCTCTCCGCGAGATCCAGTACCGGATCGAGAGAC 480
521 GCTGCTCTCAAGGCGCGCGGCTCTCTCCGCGAGATCCAGTACCGGATCGAGAGAC 580
481 CACGCGCGGCTCTCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
581 CACGCGCGGCTCTCCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 640
541 CTCCTCTCCGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAGG 600
641 CTCCTCTCCGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAGG 700
601 CGCCTCTCCGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAGG 660
701 CGCCTCTCCGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAGG 760
661 CCTGAGAGACAAGCTCCGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAG 720
761 CCTGAGAGACAAGCTCCGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAG 820
721 CCTCTCTCAAGGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAG 780
821 CCTCTCTCAAGGCGGATCATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAG 880
781 CTGCTCTCTGAGCTTCT 840
881 CTGCTCTCTGAGCTTCT 940
941 CCGGAGCGGATGAGCTTCT 900
1001 CCGGAGCGGATGAGCTTCT 1000
901 GCGGAGAGAGACCT 960
1001 GCGGAGAGAGACCT 1060
961 CCT 982
1061 CCT 1082

RESULT 2
US-08-844-274-20
; Sequence 20, Application US/08844274B
; Patent No. 6218185
; GENERAL INFORMATION:
; APPLICANT: Frazer Jr., Malcolm J.
; APPLICANT: Shick, Paul D.
; APPLICANT: Ellick, Teri A.
; APPLICANT: Perera, Omachthage
; TITLE OF INVENTION: P19gyBac Transposon-Based Genetic Transformation System
; FILE REFERENCE: 0148_96
; CURRENT APPLICATION NUMBER: US/08/844,274B
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/016,234
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 20
; LENGTH: 7560

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: p3E1.2hs/opd
US-08-844-274-20
Query Match 64.0%; Score 628.8; DB 3; Length 7560;
Best Local Similarity 77.8%; Pred. No. 1e-99;
Matches 759; Conservative 0; Mismatches 217; Indels 0; Gaps 0;
1 CGGCGGATCAACATCTCCGAGCGGCTTACCTTACCCGAGAGACATCTCGGCTC 60
1153 CGGTCTATCAACATCTTGAAGGGGTTTCACTGACATCAACAGACATCTTCGCGAG 1212
61 CTCGCGGCTTCTCTCCGCGCTGCGGAGTTCTTGCGGCTCCGCAAGGCTCGCGCA 120
1213 CTCGCGGAGATTCTTGCGGCTTGGCAGAGTTCTTGCGGCTCCGCAAGGCTCTAGCGGA 1272
121 GAAGGCGGTGCGGCTCTCGCGCGGCTCGCGCGGCGCGCGGCGGCGGCGGCGGCGG 180
1273 AAGGCTGTGAGAGATTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
181 GTCCACCTTGCACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
1333 GTCCACCTTGCACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1392
241 CGTGCACATCGTGGCCGACCGGCTCTGAGTTGCAACCGGCGGCTCTCAATGCGGCTCCG 300
1393 CGTTCAATCGTGGCCGCGGCGGCGGCTTGTGTTGCAACCGGCGGCTCTCAATGCGGCTCCG 1452
301 CTCGTGAGAGAGCTCAACCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
1453 GAGTGTAGAGAGACTCAACAGTTCTTCTGCGGAGATTCAATATGAGATCGAAGACAC 1512
361 CGGATCCGCGCGGCGGATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAGGCAAG 420
1513 CGGAATTAGGCGGCGGATCAAGATGAGCCACACCGGCAAGGCAAGGCAAGGCAAGGCAAG 1572
421 GCTGCTCTCAAGGCGGCGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
1573 GTTATGTATTAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1632
481 CACGCGGCTCTCCAGCGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 540
1633 CACGCGGCAAGGTGAGCGGATGAGTGTGAGCAGGCGGCGGCGGCGGCGGCGGCGGCT 1692
541 CTCCT 600
1693 GAGCCCTCAAGGCTTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1752
601 CGCCT 660
1753 CGCCT 1812
661 CTTGAGAGACAAGCT 720
1813 TCTAGAGATATATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1872
721 CTTCTCTATCAAGGCGGCT 780
1873 TCTCTTATCAAGGCGGCT 1932
781 CTGCT 840
1933 CTGCT 1992
841 CCGGAGCGGATGAGCTTCAATCCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
1993 CCGGAGCGGATGAGCTTCAATCCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2052
901 GCGGAGAGAGACCT 960
2053 CCGAGAGAGAGAGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2112

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Oy      961  CCTCGGCGCCTCTGA  976
        | | | | | | | |
Db      2113 CTTGCGGCGCTCATGA  2128

RESULT 3
US-09-598-421-20
; Sequence 20, Application US/09598421
; Patent No. 6551825
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcom J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Elick, Teri A.
; APPLICANT: Pereira, Onathage
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
; TITLE OF INVENTION: for Insects
; FILE REFERENCE: 0148_96
; CURRENT APPLICATION NUMBER: US/09/598,421
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 60/016,234
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 20
; LENGTH: 7560
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: p3E1.2ns/opd
US-09-598-421-20

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[illegible]

Db	1693	GAGCCCTCAGCGGTTTGTATTGTGCACAGCGATGATACCTGAGCATTTGAGCTTATCTTCAC	1752
Oy	601	CGCCCTGCGCGCCCGCGGCTAACCTCATCGGCTTCGACACATCCCGCATTCGCCCATCGG	660
Db	1753	CGCCCTGCGCGCGCGGATATCTCATCGGCTTAGACACATCCCGCACATGCGGATTTGG	1812
Oy	661	CTTCGAGACACGCTTCGCCGCTCCGCCCTCTTCGCGATCCGCTCTCGGACAGCCCGCC	720
Db	1813	TCCTGAAGATATATCGATGTCATAGCCCTCTCGGGATCCGTTCCGCGGACACCGGCG	1872
Oy	721	CCCTCTATCAAGGSCCTCATTCGACGAGGGCTATAGAGAGATCCCTCGGTCCACGGA	780
Db	1873	TCCTTTATCAAGGCGCTCATCGACGACGATACATACAAATCCCTGTTGAAATGA	1932
Oy	781	CTGSCCTTCGCGCTTCTCTCTCTACGAGACCAACATCATGGACGTGATGACCCGCTGAA	840
Db	1933	CTGSCCTTCGCGGTTTTTCGACTATGTCCACCAATCATAGCACTGATGATCCCGTGA	1992
Oy	841	CCCGGACGGCATGCGCTTTCATCCGCTCCGCGTATCCGTTCTCCGCGGAAGAGCGT	900
Db	1993	CCCGGACGGATGCGCTTTCATTCACATGAGAGTATCCCATTCCTACGAGGAGAGGCGT	2052
Oy	901	GCGCGAGAGACCTTCGCGCGGATCACCCTGACCAACCCGGGCCGCTTCTCTCCCGGAC	960
Db	2053	CCCGAGAGAAACGCTGCGACGGCATCACTGTGACATMAACCCGCGGCTTCTTGTACCGAC	2112
Oy	961	CCCTCGGCGCCTCTGA 976	
Db	2113	CTTCGCGGCGCTCATGA 2128	

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RESULT 4
5484728-1
: Patent No. 5484728
: APPLICANT: SEERDAR, CINEYT M.; MURDOCK, DOUGLAS
: TITLE OF INVENTION: PARATHION HYDROLASE ANTAGONISTS AND METHODS
: FOR PRODUCTION AND PURIFICATION
: NUMBER OF SEQUENCES: 6
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/333, 8892
: FILING DATE: 01-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 898, 973
: FILING DATE: 25-JUN-1992
: APPLICATION NUMBER: 312, 503
: FILING DATE: 17-FEB-1989
: APPLICATION NUMBER: 237, 255
: FILING DATE: 26-AUG-1988
: SEQ ID NO.:1
: LENGTH: 1341
5484728-1

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Query Match	63.9%;	Score 627.2;	DB 6;	Length 1341;
Best Local Similarity	77.7%;	Pred. No. 1.8e-99;		
Matches 758;	Conservative 0;	Mismatches 218;	Indels 0;	Gaps 0;
QY	1	CGGCCGATCCATCTTCGAGCGCGGCTTCACTTACCTTACCTCCAGAGCAATCTGGGCTC	60	
DB	189	CGGTCTATCAATCTCTGAAAGCGGGTTTCACTGACTCAACAGACAATCTTCGGCGAG	248	
QY	61	CTCGCGCGGCTCTCTCGCGCGCTGCGCGGAGTTTGTGGGCTCCGCAAGGCGCTCGCGCA	120	
DB	249	CTCGCGAGATTTCTTGCGTCTTGGCCAGAGTTCTTGGTAGCCGCAAGCTCTTAGCGGA	308	
QY	121	GAAAGCGGTGCGCGGCTCTCGCGCGCGCGCGCGCGCGCGGTGCGCAACATGTGAGCT	180	
DB	309	AAAGGCTGTAGAGAAATTTGCGCGCGCGCAAGAGCGGTGCGTGGAAAGATTTGTGATGT	368	
QY	181	GTCAACCTTGCAACTCGGCGCGGCAAGTGTCCCTCTCGGCGGAAGTGTCCGCGCGCCGA	240	
DB	369	GTCAACCTTGCAATTCGGTTCGGACAGTCAAGTTTATGTGGCCGAAGTTTTCGCGGCTGCGCA	428	

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QY 241 CTTGCAATCTGTGCGCCGACCGGCTCTGTGATCCCGCGCTCTCCATGCGCTCCG 300
D 429 CGTTCTATCTGTGGGCGGACCGGCTGTGGTTCCACCCGCCACTTTCGATGCGATTGAG 488
QY 301 CTCGGTAGAGAGCTCACCCAGTTCTTCTCCGGAGATCCAGTACGGCATCGAGAGAC 360
D 489 GAGGTAGAGAACTCACAGATTTCTTCTGCTGAGATTCATATGGCATGGAAGACAC 548
QY 361 CGGCATCCGCGCGCATCATCAGGTGGCCACACCGGCAAGGCCACCCGTTCCAGGA 420
D 549 CGGAATTAGGGCGGCAATTATCAAGTGGCCACACAGGCAAGGAGACCCCTTTCAAGA 608
QY 421 GCTGTCTCAAGCGCGCGCGCGCTCTCCCTCGCCACCGCGTGGCGGTGATCCACCA 480
D 609 GTTAGTGTAAAGGCGCGCGCGCGCCAGCTTGCCCAACGGTGTTCGGTAAACACTCA 668
QY 481 CACCGCGCTCTCCGCGGAGCGGAGACGAGAGCGCCGCACTTCCGATCCGAGGCGCT 540
D 669 CACGCAAGCAAGTCAAGCGGATGTAGAGAGAGCGCCGCAATTTTGAGTCCGAAGGCTT 728
QY 541 CTCCTCGTCCGCGTGTGATCGGCACTCCGACGACACCGAGCACTCTCCATCTCAC 600
D 729 GAGCCCTCAAGGGTTTGTATTTGTCACAGGATGATCTGACGATTTGAGCTATCTCAC 788
QY 601 CGCCTCGCGCGCGCGCTACCTCATGCGCTCGACCAATCCGCACTCCGCACTCCGATCG 660
D 789 CGCCTCGCTCGCGCGGATACCTCATGCTGTAGACCAATCCGCAACAGTGCATTGG 848
QY 661 CTTGAGAGCAACGCTCCGCGTCCGCTCGGCACTCCGCTCGGCAAGCCGCGC 720
D 849 TCTAGAGATTAATGCGATGCTACAGCCCTCTGCGGCACTCGTTGTGCAAAACGCGGC 908
QY 721 CTTCTCATCAAGGCTCATCGACAGGCTACATGAGAGATCTTGTGTCCACGA 780
D 909 TCTCTGATCAAGGCGCTCATCGACCAAGGCTACATGAAACAAATCTCTGTGAAATGA 968
QY 781 CTGCTCTTGGGCTTCTCTCTAGTGAACCAATCATGAGCGTATGAGACCGGCTGA 840
D 969 CTGCTGTGCGGTTTTCAGAGTATGTCAACCAATCATGAGCGTATGAGTATGCGGTGA 1028
QY 841 CCGGAGCGGATGCGCTTATCCGCTCGGCTGATCCGCTTCTCCGCGAAGAGGCGT 900
D 1029 CCGGAGCGGATGCGCTTATCCGCTCATGAGTATCCATTTCTTCAAGAGAGAGGCGT 1088
QY 901 GCGGAGAGAGACCTTCGCGCGGATCAGCGTGAACCAACCGCGCTTCTCTCCGAC 960
D 1089 CCGCAGAGAAACGCTGCGAGGCACTGTGACTTAACCCGCGGCGGTTCTGTACCGAC 1148
QY 961 CTTCCGCGCTCTCTGA 976
D 1149 CTTGCGGCGTCAATGA 1164
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RESULT 5
5484728-1
; Patent No. 5484728
; APPLICANT: SEERDAR, CUNEYT M.; MURDOCK, DOUGLAS
; TITLE OF INVENTION: PARATHION HYDROLASE ANALOGS AND METHODS
; FOR PRODUCTION AND PURIFICATION
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333, 8892
; FILING DATE: 01-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 898, 973
; FILING DATE: 25-JUN-1992
; APPLICATION NUMBER: 312,503
; FILING DATE: 17-FEB-1989
; APPLICATION NUMBER: 237,255
; FILING DATE: 26-AUG-1988
; SEQ ID NO: 1:
; LENGTH: 1341
5484728-1
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Query Match 63.9%; Score 627.2; DB 6; Length 1341;
Best Local Similarity 77.7%; Pred. No. 1.8e-99;
Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 1 CCGCCCATCAACATCTCCAGGCGCGCTTACACCTTACACCAAGAGCATCTGGGCTC 60
D 189 CGGTCTTATCAACATCTCTGAAGCGGTTTACACTGACTACAGACCATCTTGGCGAG 248
QY 61 CTCGCGCGCTTCTCCGCGCTGAGGAGTCTTTCGAGCTCCGCAAGGCGCTCGCGCA 120
D 249 CTCGCGAGAGATTCTTGGCTGCTTGGCCAGAGTTCTTCGATGCGGCAAGGCTTAAGCG 308
QY 121 GAAGCGCTGCGCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
D 309 AAGGCTGTGAGAGATTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 368
QY 181 GTCCACTTGCACATCGGCGCGGACGTCTCTCGCGGAGGTGTCGCGCGCGCGCGCG 240
D 369 GTCCACTTGCATCTCGGTGCGGAGTCAATTTAGCGAGGTTTCGCGGCGTGGCGA 428
QY 241 CTTGCAATCTGTGCGCGGCAACGCGCTGTGATGACCGCGGCTCTCATGCGGCTCG 300
D 429 CGTTCTATCTGTGCGCGGAGACCGGCTGTGATGACCGGCACTTTGATGCAATTGAG 488
QY 301 CTCCTGAGAGAGCTCAACCAATTCTTCTCCGGAATTCAGTACGCGATGAGAGAC 360
D 489 GAGTGTAGAGAACTCACACAGTTCTTCTCGTGAATTCATATGAGCATGAAAGAC 548
QY 361 CCGCATCCGCGCGCGGATCATCAGGTGGCCACCAACCGGCAAGGCCACCCGTTCCAGGA 420
D 549 CGGAATTAGGGCGGCAATTAAGTGTGCAACCAAGGCAAGGCAAGCCCTTTTCAAGA 608
QY 421 GCTGTGCTCAAGGCGCGCGCGCTCTCGGCAACCGGCTGCGGATGACCAACCA 480
D 609 GTTAGTGTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 668
QY 481 CACGCGCTCTCCAGCGGAGCGGAGCAGCAGGCGCGCATCTTGAATCGAGGCGCT 540
D 669 CACGCAAGCAAGTCAAGCGGATGTGAGCAGGCGCGCATTTTGTAGTCCGAAGGCTT 728
QY 541 CTCCTCGTCCGCGTGTGATCGGCACTCCGCAACCGGCTGCGGATGACCAACCA 600
D 729 GAGCCCTCAAGGCTTGTATGTGTCACAGGATGATATGACATTTGAGCTATCTTAC 788
QY 601 GCGCCTCGCGCGCGGCTACCTCATGCGGCTCGACCAATCCGCACTCCGCACTCG 660
D 789 CGCCTCGCTCGCGCGGATACCTCATGCTGTGATGACCAATCCGCACTAGTGG 848
QY 661 CTTGAGAGCAACGCTTCGCGGCTCGGCTCTCGGCAATCGGCTCTGAGACCGCGC 720
D 849 TCTAGAGATTAATGCGATGCTACAGCCCTCTGGGCACTCGTTCTGTGCAAAACGCGG 908
QY 721 CTTCTCATCAAGGCTCATCGACAGGCTTATGAGAGATCTCTGTGTCCACGA 780
D 909 TCTCTTATCAAGGCGCTCATCGACCAAGGCTTATGAAACAAATCTCTGTGAAATGA 968
QY 781 CTGCTCTTGGGCTTCTCTCTAGTGAACCAATCATGAGCGTATGAGACCGGCTGA 840
D 969 CTGCTGTGCGGTTTTCAGAGTATGTTCACCAATCATGAGCGTATGAGTATGCGGTGA 1028
QY 841 CCGGAGCGGATGCGCTTATCCGCTCGGCTGATCCGTTCTCTCCGCGAAGAGGCGT 900
D 1029 CCGGAGCGGATGCGCTTATCCGCTCATGAGTATCCATTTCTTCAAGAGAGGCGT 1088
QY 901 GCGGAGAGAGACCTTCGCGCGGATCAGCGTGAACCAACCGCGCTTCTCTCCGAC 960
D 1089 CCGCAGAGAAACGCTGCGAGGCACTGTGACTTAACCCGCGGCGGTTCTGTACCGAC 1148
QY 961 CTTCCGCGCTCTCTGA 976
D 1149 CTTGCGGCGTCAATGA 1164
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RESULT 6
US-09-603-450-3
; Sequence 3, Application US/09603450
; Patent No. 6469145
; GENERAL INFORMATION:
; APPLICANT: Raetlogi, Vapin K
; APPLICANT: Cheng, Tu-c
; APPLICANT: Defrank, Joseph J
; TITLE OF INVENTION: One-Step Purification Process for Organophosphorus
; TITLE OF INVENTION: Hydrolyase Enzyme
; FILE REFERENCE: DAM-508-99
; CURRENT APPLICATION NUMBER: US/09/603,450
; CURRENT FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1693
; TYPE: DNA
; ORGANISM: Flavobacterium sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (506)..(1516)
; OTHER INFORMATION: Expresses organophosphorus hydrolase
; NAME/KEY: sig peptide
; LOCATION: (419)..(505)
; OTHER INFORMATION: Removal of signal peptide allows organophosphorus
; OTHER INFORMATION: hydrolase to be expressed in soluble form
US-09-603-450-3

Query Match 63.9%; Score 627.2; DB 3; Length 1693;
Best Local Similarity 77.7%; Pred. No. 1.8e-99;
Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 1 CGGCCGATACCATCTCCGAGCGCGCTTCACTCCACCGAGACATCTCGCGCTC 60
DB 541 CGGCTCTATCAAACTCTGAAAGCGGTTTCACTGACATCTCGCGCGAG 600
QY 61 CTCGCGCGCTTCTCCGCGCTGCGCGAGTTCTTCGCGCTCCGAAAGCCCTCGCGA 120
DB 601 CTCGCGAGATCTTGGCGCTTGGCGAGTTCTTCGCGAGCGGAAAGCTCTGAGCGGA 660
QY 121 GAAGCGCGCTGCGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 661 AAAGCGCTGAGAGGATTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 181 GTCCACTTTCGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 721 GTTCGACTTTCGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 241 CGTGCACATCG 300
DB 781 CGTTATATCG 840
QY 301 CTCGCGAGAGCTCAACCAAGTTCTTCGCGCGAGATCCAGTACGAGGATCGAGGAC 360
DB 841 GAGGTAGAGAACTCAACAAGTTCTTCGCGCGAGATCCAGTACGAGGATCGAGGAC 900
QY 361 CGGCAATCG 420
DB 901 CGGAATTAAGGCG 960
QY 421 GCTCGTCTCAAGCG 480
DB 961 GTTAGGTAAAGCG 1020
QY 481 CACCGCGCGCTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
DB 1021 CACGCGAGAACTCAAGGATTTGAGAGCGAGCGCGCGCGCGCGCGCGCGCGCG 1080
QY 541 CTCGCGCGCTCG 600
DB 1081 GAGCCCTCACGGGTTTGTATGGTCAAGCGATGATGAGATTTGAGCTATCTCAC 1140

QY 601 CGCCTCCGCGCGCGCGCTACTTCATCGGCGCTCGACCAATCCGCACTCGCCATCG 660
DB 1141 CGCCTCCGCGCGCGCGGATTAAGTCTGAGTCTGAGACCAATCCGCGCAAGTGG 1200
QY 661 CTTGAGAGCAACGCTCCGCGCTCCGCGCTCTCGCGATTCGCTCTCGCGACCGCG 720
DB 1201 TCTAGAAATATAGGAGTGCATTCAGCCCTCTCGCGCATTCGCTTCGCGAAACGCG 1260
QY 721 CTTCTCATCAAGCGCTTCATCGACGAGGCTACATGAGAGATCTCGTTCACAGA 780
DB 1261 TCTTGTATCAAGCGCTTCATCGACGAGGCTACATGAGAGAAATCTCTGTTCAGAT 1320
QY 781 CTGCTCTTGGCTTCTCTCTCTAGTACCAATATGAGATGAGACCGCGTGA 840
DB 1321 CTGCTCTTGGGTTTTCAGATATGTCAACCAATATGAGATGAGATCGGCTGA 1380
QY 841 CCGGACGCGATGCGCTTCATTCGCGCTCGCGCTGATTCGCTTCGCGAGAGGCGT 900
DB 1381 CCGGACGCGATGCGCTTCATTCGCGCTGATTCGCGCTGATTCGCGAGAGGCGT 1440
QY 901 GCGGAGAGAACCTTCGCGCGATGACGCGAACCGCGCGCTTCGCGCGAG 960
DB 1441 CCGACAGAAACGCTGCGAGGATGACGCGAACCGCGCGCTTCGCGAGAG 1500
QY 961 CTTGCGCGCTCTGA 976
DB 1501 CTTGCGCGCTGATGA 1516

RESULT 7
US-08-844-274-14/c
; Sequence 14, Application US/08844274B
; Patent No. 6218185
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcolm J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Ellick, Teri A.
; APPLICANT: Perera, Omachage
; TITLE OF INVENTION: Piggybac Transposon-Based Genetic Transformation System
; TITLE OF INVENTION: for Insects
; FILE REFERENCE: 0148.96
; CURRENT APPLICATION NUMBER: US/08/844,274B
; CURRENT FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/016,234
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 14
; LENGTH: 6723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: piggyBac/opd
US-08-844-274-14

Query Match 63.9%; Score 627.2; DB 3; Length 6723;
Best Local Similarity 77.7%; Pred. No. 1.9e-99;
Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 1 CGGCCGATACCATCTCCGAGCGCGCTTCACTCCACCGAGACATCTCGCGCTC 60
DB 4194 CGGCTCTATCAAACTCTGAAAGCGGTTTCACTGACATCTCGCGCGAG 4135
QY 61 CTCGCGCGCTTCTCCGCGCTGCGCGAGTTCTTCGCGCTCCGAAAGCCCTCGCGA 120
DB 4134 CTCGCGAGATCTTGGCGCTTGGCGAGAGTTCTTCGCGTACCGCGAAAGCTTACGCGA 4075
QY 121 GAAGCGCGCTGCGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 4074 AAAGCGCTGAGAGATTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4015
QY 181 GTTCACCTTTCGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240

Db 4014 GTGACCTTTCATATCGTGGAGCTCACTTATTTGGCGGCTTCCGCGGCTGCGCA 3955
Qy 241 CGTGACATTCGTGGCGCCAGCCGCTCTGTTCCAGCCCGCTCTCCATGCGCTCCG 300
Db 3954 CGTTATATCGTGGGCGGAGCCGGCTTGTTGTTCCAGCCCGCATCTTCATGCAATGAG 3895
Qy 301 CTCCTGAGAGACTCAACCACTTCTCTCCGAGATCCAGTACGAGATGAGACAC 360
Db 3894 GAGTATAGAGAACTCACACACTTCTCTCCGAGATCCAGTACGAGATGAGACAC 3835
Qy 361 CGGCATCCGCGCGCATATCAAGTGGCCACACCCGCAAGGCCACCCCTTCCAGA 420
Db 3834 CGGAATTAGGGGCGCATTTATCAAGTCCGACACAGGCAAGGAGACCCCTTCCAGA 3775
Qy 421 GCTGCTCAAGAGCGCGCGCGCGCTCTCCGCAACCGCGAGTGGCGGATCCAGCA 480
Db 3774 GTTATGTTAAAGGGGCGCGCGCGCGCGCTTGGCCACCGGTTTCCGATACCACTCA 3715
Qy 481 CACCGCGCTCTCCAGCGCGAGCGAGCAAGAGCGCGCATCTTCCAGTCCGAGGGCT 540
Db 3714 CACGCGAGCAAGTCAAGCGGATGATGAGAGAGCGCGCATTTTGAAGTCCGAAGGCTT 3655
Qy 541 CTCGCCGTCGCGGATGATGAGAGCGCATCCGACAGACCGCATCTCTACCTCAAC 600
Db 3654 GAGCCCTCAAGGTTTGTATGTTCAAGCGATGATGAGATGAGCTATCTCAC 3595
Qy 601 CGCCCTCGCGCGCGCGCTACCTCATCGGCTCGACCAATCCGCACTCCGCAATCGG 660
Db 3594 CGCCCTCGCGCGCGCGGATCTCATCGGCTCAACCAATCCGCAAGTGGCATTTGG 3535
Qy 661 CTTGAGAGCAAGCGCTCGCGCTCGGCTCTCTCGAGATCGGCTCTCGAGACCGCGC 720
Db 3534 TCTAAGATATATGAGATGATCAAGCCCTCTGCGGCAATCCGTTGTTGAAAGCA 3475
Qy 721 CTTCTCATCAAGCGCTCATGACCAAGGCTCAATGAAGATCTCTGTTCCAAAGA 780
Db 3474 TCTCTTATCAAGGCGCTCATGACCAAGGCTCAATGAAGATCTCTGTTGAAAGCA 3415
Qy 781 CTGCTCTTCCGCTTCTCTCTCAAGTACCAATGAGATGAGATGAGACCGGTTAA 840
Db 3414 CTGGCTGTTCCGGGTTTGAAGTATGTCACCAATCAATGAGATGAGATGAGATGAA 3355
Qy 841 CCGGAGCGCATGCTTCATTCGCGCTCGCGCTGATCCGCTCTCTCGAGAGAGGCT 900
Db 3354 CCGGAGCGGATGCTTCATTCGCGCTGATCCGCTGATCCGCTCTCTCGAGAGAGGCT 3295
Qy 901 GCGGAGAGAGCCCTCGCGGATACCGTACCAACCGCGCGCTCTCTCTCGAGAG 960
Db 3294 CCGGAGAGAGAGCGTGGAGGATCACTGATCAACCGCGCGCTCTCTCTCGAGAG 3235
Qy 961 CTTCCGCGCTCTCTGA 976
Db 3234 CTTGGCGGCGTCAATGA 3219

RESULT 8
US-09-598-421-14/c
Sequence 14, Application US/09598421

Patent No. 6551825
GENERAL INFORMATION:

APPLICANT: Frazer Jr., Malcom J.
APPLICANT: Shirk, Paul D.

APPLICANT: Ellick, Teri A.
APPLICANT: Pereira, Omalchage

TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
TITLE OF INVENTION: for insects

FILE REFERENCE: 0148.96
CURRENT APPLICATION NUMBER: US/09/598.421

PRIOR APPLICATION NUMBER: 2000-06-19
PRIOR FILING DATE: 1996-04-19

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0 - beta
SEQ ID NO 14
LENGTH: 6723
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES: Description of Artificial Sequence: piggyBac/opd
US-09-598-421-14
Query Match
Beet Local Similarity 77.7%; Pred. No. 1.9e-99;
Matches 758; Conservative 0; Mismatches 218; Indels 0; Gaps 0;
Qy 1 CGGCCGATCAACATCTCCAGGCGCGCTTCAACCTCAACCAAGACATCTGCGCTC 60
Db 4194 CGGTCCTATCAACATCTCCAGGCGCGCTTCAACCTCAACCAAGACATCTGCGCGAG 4135
Qy 61 CTCGCCGCTTCTCCGCGCTGCGCGAGTCTTCCGCTCCGCAAGGCTCTGCGCA 120
Db 4134 CTCGCCGAGATCTTCCGCGCTTCCGCGAGTCTTCCGCGCAAGGCTCTGAGCGGA 4075
Qy 121 GAAGCGGTGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 4074 AAGGCTGTGAGAGATTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4015
Qy 181 GTCACTTTCGACATCGGCGCGCGAGTGTCTCTCTCGAGAGTGTCCGCGCGCGCA 240
Db 4014 GTGACCTTTCATATCGTGGAGCTCACTTATTTGGCGGCTTCCGCGGCTGCGCA 3955
Qy 241 CGTGACATTCGTGGCGCCAGCCGCTCTGTTCCAGCCCGCTCTCCATGCGCTCCG 300
Db 3954 CGTTATATCGTGGGCGGAGCCGGCTTGTTGTTCCAGCCCGCATCTTCATGCAATGAG 3895
Qy 301 CTCCTGAGAGACTCAACCACTTCTCTCCGAGATCCAGTACGAGATGAGACAC 360
Db 3894 GAGTATAGAGAACTCACACACTTCTCTCCGAGATCCAGTACGAGATGAGACAC 3835
Qy 361 CGGCATCCGCGCGCATATCAAGTGGCCACACCCGCAAGGCCACCCCTTCCAGA 420
Db 3834 CGGAATTAGGGGCGCATTTATCAAGTCCGACACAGGCAAGGAGACCCCTTCCAGA 3775
Qy 421 GCTGCTCAAGAGCGCGCGCGCTCTCCGCAACCGCGAGTGGCGGATCCAGCA 480
Db 3774 GTTATGTTAAAGGGGCGCGCGCGCGCGCTTGGCCACCGGTTTCCGATACCACTCA 3715
Qy 481 CACCGCGCTCTCCAGCGCGAGCGAGCAAGAGCGCGCATCTTCCAGTCCGAGGGCT 540
Db 3714 CACGCGAGCAAGTCAAGCGGATGATGAGAGAGCGCGCATTTTGAAGTCCGAAGGCTT 3655
Qy 541 CTCGCCGTCGCGGATGATGAGAGCGCATCCGACAGACCGCATCTCTACCTCAAC 600
Db 3654 GAGCCCTCAAGGTTTGTATGTTCAAGCGATGATGAGATGAGCTATCTCAC 3595
Qy 601 CGCCCTCGCGCGCGCGGCTACCTCATCGGCTCGACCAATCCGCACTCCGCAATCGG 660
Db 3594 CGCCCTCGCGCGCGCGGATCTCATCGGCTCAACCAATCCGCAAGTGGCATTTGG 3535
Qy 661 CTTGAGAGCAAGCGCTCGCGCTCGGCTCTCTCGAGATCGGCTCTCTCGAGAGAGGCT 900
Db 3534 CCGGAGAGAGAGCGTGGAGGATCACTGATCAACCGCGCGCTCTCTCTCGAGAGAGGCT 3295
Qy 901 GCGGAGAGAGCCCTCGCGGATACCGTACCAACCGCGCGCTCTCTCTCGAGAG 960
Db 3294 CCGGAGAGAGAGCGTGGAGGATCACTGATCAACCGCGCGCTCTCTCTCGAGAG 3235
Qy 961 CTTCCGCGCTCTCTGA 976
Db 3234 CTTGGCGGCGTCAATGA 3219

Qy 901 GCCGAGAGACCTTCGCGGATCATCCGTGACCAACCCGCGCTTCCTCCCGAC 960
Db 3294 CCCAGAGAAACGCTGGCAGGATCATCTGTACTAACCCGCGCGCTTCCTGACCGAC 3235
Qy 961 CCTCGCGCTTCCTGCA 976
Db 3234 CTGCGGCGCTCATGA 3219

RESULT 9

US-08-844-274-13
; Sequence 13, Application US/08844274B
; Patent No. 6218185
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcom J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Ellick, Teri A.
; APPLICANT: Perera, Omachhage
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
; FILE REFERENCE: 0148.96
; CURRENT FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/016,234
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 13
; LENGTH: 6723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Clone p3el.2H/S
US-08-844-274-13

Query Match 63.5%; Score 624; DB 3; Length 6723;
Best Local Similarity 77.5%; Pred. No. 6.7e-99;
Matches 756; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 1 CGGCCCCATCAACATCTCCGAGCGCGCTTCACCTTACCCAGGACATCTGGGCTC 60
Db 2530 CGGTCTATCAACATCTCTGAAGCGGGTTTCACTGACATCTGCGGAG 2589
Qy 61 CTCGCGCGCTTCCTCCGCGCTTCGCGAGTTCTTCGGCTCCCGCAAGGCGCTCGCGA 120
Db 2550 CTCGCGAGATTCCTGCTGCTTCGCGAGTTCTTCGGTACCGCAAGCTCTAGCGGA 2649
Qy 121 GAAGGCGCTGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 2650 AAAGGCTGTGAAGATTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2709
Qy 181 GTCCACCTTCGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 2710 GTCCACTTTCATATCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2769
Qy 241 CGTGACATCTGCG 300
Db 2770 CGTTATATCTGCG 2829
Qy 301 CTCGCTGAGAGCTCACCGAGTTCTTCCTCCGAGATCGATCGGATCGAGAAC 360
Db 2830 GAGGTAGAGAACTCACACAGTTCTTCCTGCTGAGATTCATATGCGATGGAAGAC 2889
Qy 361 CGGACATCG 420
Db 2890 CGGAATTAGGCG 2949
Qy 421 GCTCGTCTCAAGCG 480
Db 2950 GTTATGTTAAAGCG 3009
Qy 481 CACCGCGCTTCAGCG 540
Db 481 CACCGCGCTTCAGCG 540

Db 3010 CACGAGCAAGTACGCGCGATGCTGAGCAGACAGCGCGCATTTTGTGATCGAAGCTT 3069
Qy 541 CTCGCCGTCGCGCGGATCGGCGCACTCCGAGCAACCGACGACCTCTCTACCTGAC 600
Db 3070 GAGCCCTTACGCGGTTTGTATGATGATGATGATGATGATGATGATGATGATGAT 3129
Qy 601 CGCCCTGCG 660
Db 3130 CGCCCTGCTGCG 3189
Qy 661 CTGAGAGCAACGCTTCGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db 3190 TCTAGAGATATATGAGTGCATCAGCGCTTCGCGCGCGCGCGCGCGCGCGCGCG 3249
Qy 721 CCTCTCATCAAGGCG 780
Db 3250 TCTCTGATCAAGGCG 3309
Qy 781 CTGCTCTTCGCGCTTCCTCTCTACGTCGACCAATCATGAGCGATGAGACCGCGTAA 840
Db 3310 CTGCTGTTGGGTTTTCGACTATGTCACCAACATCATGAGCGATGAGATCGCGTAA 3369
Qy 841 CCGGACGCGATGCGCTTCATCCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 3370 CCGGACGCGATGCGCTTCATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3429
Qy 901 GCCGAGGAGACCGTCG 960
Db 3430 CCACAGAAACGCTGCGAGGATCATCTGATCACTAACCGCGCGCGCTTCTGTACCGAC 3489
Qy 961 CCTCGCGCTTCCTGCA 976
Db 3490 CTGCGGCGCTCATGA 3505

RESULT 10

US-09-598-421-13
; Sequence 13, Application US/09598421
; Patent No. 6551825
; GENERAL INFORMATION:
; APPLICANT: Fraser Jr., Malcom J.
; APPLICANT: Shirk, Paul D.
; APPLICANT: Ellick, Teri A.
; APPLICANT: Perera, Omachhage
; TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
; FILE REFERENCE: 0148.96
; CURRENT FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/016,234
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 13
; LENGTH: 6723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Clone p3el.2H/S
US-09-598-421-13

Query Match 63.5%; Score 624; DB 4; Length 6723;
Best Local Similarity 77.5%; Pred. No. 6.7e-99;
Matches 756; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 1 CGGCCCCATCAACATCTCCGAGCGCGCTTCACCTTACCCAGGACATCTGGGCTC 60
Db 2530 CGGTCTATCAACATCTCTGAAGCGGGTTTCACTGACATCTGCGGAG 2589
Qy 61 CTCGCGCGCTTCCTCCGCGCTTCGCGAGTTCTTCGGCTCCCGCAAGGCGCTTCGCGA 120
Db 2550 CTCGCGAGATTCCTGCTGCTTCGCGAGTTCTTCGGTACCGCAAGCTCTAGCGGA 2649

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QY 121 GAAGCCGTCGCGCCCTCCGCGCGCCGCGCGCGCTGCGCACATCTGAGAGT 180
D 2550 AAAAGCTGTGAGAGATTGCGCGCGCCGAGCGGCTGGCGGCAAGATTGTGATGT 2709
QY 181 GTCCACCTTGCACATCCGCGCGCGAGTGTCCCTCTCCGCGAGGTTGCCGCGCGCA 240
D 2710 GTCCACCTTGCATCTGATCTGCGCGAGCTGATTTATTTGCGCGAGGTTGCGCGCGCA 2769
QY 241 CGTGACATCTGTGCGCGCGCACCGGCTCTGTTGACCGCGCGCTCTCATGCGCTCG 300
D 2770 CGTTGATATCGTGGCGCGGACCGGCTGTGTTGATGACCGCGCATTTGATGCAATTAG 2829
QY 301 CTCGCTGAGAGACTCACCCAGTTCTTCTCCGCGAGATCCAGTACGCGCATGAGACAC 360
D 2830 GAGTGTAGAGAACTCACACAGTTCTTCTCTCGTGAATTCAATTGCGCATGAAAGACAC 2889
QY 361 CGGATCCGCGCGCGCGCATCATCAAGGTGCGCACCGCGCAAGGCGCACCGCTTCCAGA 420
D 2890 CGAAATTAGGCGCGCGCATTTATCAAGTGTGCGCACCGCGCAAGGCGCACCGCTTCCAGA 2949
QY 421 GCTGCTCTCAAGCGCGCGCGCGCGCGCTCCCTCGCGCACCGCGCGGTGACCGCA 480
D 2950 GTTAGTGTAAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 3009
QY 481 CACGCGCGCTTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 540
D 3010 CACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3069
QY 541 CTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 600
D 3070 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3129
QY 601 CGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 660
D 3130 CGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3189
QY 661 CTTGAGAGACAAGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
D 3190 TCTGAAATATATATGAGATGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3249
QY 721 CCTCTCATCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
D 3250 TCTCTTATCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3309
QY 781 CTGCTCTTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
D 3310 CTGCTGCTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3369
QY 841 CCGCGAGCGCATGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
D 3370 CCGCGAGCGCATGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3429
QY 901 GCGCGAGGAGACCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 960
D 3430 CCGCGAGGAGACCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3489
QY 961 CTTCTCGCGCGCTCTCTGA 976
D 3490 CTTCTCGCGCGCTCTCTGA 3505

RESULT 11
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
```

```
; CURRENT APPLICATION NUMBER: US/09/103, 840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 16.9%; Score 166.4; DB 3; Length 4403765;
Best Local Similarity 55.5%; Pred. No. 4e-20;
Matches 382; Conservative 0; Mismatches 276; Indels 30; Gaps 2;

QY 1 CGGCGCGATCCATCTTCCGAGCGCGGCTTCACTTCACTTCACTTCACTTCACTTCACT 60
D 276050 CGGACCGCATCGACACCGCTGATCTCGGCGTCACTGATGACGACGATCTTCACTAT 275991
QY 61 CTCGCGCGGCTTCTCCGCGCGCTGCGCGGAGTTTCTGCGCTCCGCGAGGCTTCCGCG 120
D 275990 GACCGCGAGTTGCGCGAGAACTTACCGGAGCTTGGGCGACAGGACAAAGCGGTTGC 275931
QY 121 GAAGCGCGTGGCGGAGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
D 275930 CGGCGCGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 275871
QY 181 GTTCACTTGCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
D 275870 CACGCTGATCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275811
QY 241 CGTGCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 300
D 275810 GCTAACAATCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275751
QY 301 CTCGCT-----GAGGAGCTCACCCAGTTCTTCTCTCG 333
D 275750 CTACTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275691
QY 334 CGAATTCATGATCGCGCATCGAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 393
D 275690 CGAATTCATGATCGCGCATCGAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 275631
QY 394 CACCGCGAGGCG---CACCGCGTTCAGAGCTGTCTCAAGGCGCGCGCGCGCGCGCTC 450
D 275630 CGAAGAACCGCGCGCTCACCGCTGTGTGAGCGGCGGTGCGCGCGCGCGCGCGCA 275571
QY 451 CCTCGCGACCGCGCGTGCCTGCGTGAACCAACACCGCGCGCTCCGCGCGCGCGCGAGCA 510
D 275570 CAAACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGA 275511
QY 511 GCAGCGCGCATCTTTCAGATCCAGGCGCTTCCCGCTCCGCGGTGATCGGCGCACTC 570
D 275510 CCAAGCAAGCATCTTTCGCGCGAGAGGCGGTGACTTGAAGCGGCGGTGATCGGCACTG 275451
QY 571 CGAGGACACCGACGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 630
D 275450 CGGCGACGACCGACGATCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 275391
QY 631 CTTGACGACATCTCCGCGCATCTCGCGCATC 658
D 275390 GATGACCGGTTCCGCGCATCTCGCGCATC 275363

RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
```

APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 16.9%; Score 166.4; DB 3; Length 4411529;
Best Local Similarity 55.5%; Pred. No. 4e-20;
Matches 382; Conservative 0; Mismatches 276; Indels 30; Gaps 2;

Qy 1 CGGCGGATTCACATCTCCGAGCGCGCTTCACTCCCTACCCGACGACATCTGGCGCTC 60
Db 275938 CGGACCCATCGACACCGCTGATCTCGCGTCAAGTACGACGACGATCTTCATCAT 275879
Qy 61 CTCGCGCGGCTTCTCCGCGCGCTGCGGAGTTCTTCGCGCTCCGCGAAGGCCCTGCGCGA 120
Db 275878 GACCCCGAGATGCGCGAGAACTACCGGAGCTTGGGCGACGAGACGAGCGGCTGCG 275819
Qy 121 GAAGCGCGTGGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 275818 CGGCGCGATCGCGCGCTGAGGAACTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 275759
Qy 181 GTCCACCTTCCGACATCG 240
Db 275758 CAGCGTATCG 275699
Qy 241 CGTGCATCTGCG 300
Db 275698 GCTGACATCTGCG 275639
Qy 301 CTCGCT-----GAGAGACTACCCAGTTCTTCTCTCG 333
Db 275638 CTACTCGGCG 275579
Qy 334 CGAGATTCAGTACG 393
Db 275578 CGACATCGACG 275519
Qy 394 CACCGGCAAGC---CACCGCGTTCAGGAGCTCGTCAAGCGCGCGCGCGCGCGCGCTC 450
Db 275518 CGAGCAACCGCGCGCTCACTCGTGTGTGAGCGGCTTGGCGCGCGCGCGCGCG 275459
Qy 451 CCTCGCACCGCGCGTGGCGGTGACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510
Db 275458 CAACGACACCG 275399
Qy 511 GCAAGCGCGCTTCTCGAGTCCGAGGCGCTTCCCGCTCCCGCTGTGATGGCGCATC 570
Db 275398 CGAGACGCGATCTTTCGCGAGAGGCGGTGACCTGAGCGCGGTATGGAACA 275339
Qy 571 CGACGACACCGACGCTCTCTACCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 630
Db 275338 CGGCGACGACG 275279
Qy 631 CCTGACCAATCCGCGACTCCGCCATC 658
Db 275278 GATGACCGGTTCCGCGTGAAGTATC 275251

RESULT 13
US-09-249-585A-4
Sequence 4, Application US/09249585A

Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/00905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 4
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein Barr Virus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1926)
OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

Query Match 14.0%; Score 137; DB 3; Length 1926;
Best Local Similarity 48.8%; Pred. No. 3.4e-15;
Matches 464; Conservative 0; Mismatches 475; Indels 12; Gaps 3;

Qy 32 ACCCTCACCCAGACACATCTGCGGCTCTCCGCGGCTTCTCCGCGCGCGCGCGCGAG 91
Db 117 ACCTGCTCTGCGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 176
Qy 92 TTTCTTGGCTCCCGCAAGGCGCTCCGCGAGAAAGCGGTGCGGCGCTCCGCGCGCGCG 151
Db 177 GAGTCTGATCCCGGCTTGTATCTTACACAGGCGCTTGGGCTTTTGGCAGTTCAAC 236
Qy 152 GCGCGCGGCGCGCGACCATGATGTGACGCGTAC--CTTGCATCTGCGCGCGCGAGT 209
Db 237 GTAAACGAGTTTCTCTGAGGTGCACTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 296
Qy 210 CCTCTCTGCGCGAGGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 269
Db 227 GTAAACGAGTTTCTCTGAGGTGCACTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 296
Qy 227 TGTCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 356
Db 270 GGTGAGCGCGCGCTCTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 329
Qy 357 TCCCGGCTCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
Db 330 TCCGCGAGTTCAGTACGCGATCGAGGACACCGCGATCGCGCGCGCGCGCGATCAAGT 389
Qy 417 TCTTCCCGCTCTGCT 476
Db 390 CCACCAACCGCGCAAGCGCACCGCGTTCAGAGCTGTGTCAAGCGCGCGCGCGCGCGCT 449
Qy 477 TCTCTCTCCCGTCT 536
Db 450 CCTTGCACCGCGGCTGCGGTGACCAACCGCGCGCGCGCTTCCAGCGCGCGCGAGC 509
Qy 537 TCCCGGCTCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 596
Db 510 AGCAGCGCGCATCTTTCAGTCCGAGGCGTCTCCCGTCCCGCGGTGAGTCCGCGACT 569
Qy 597 TCTTCCCGTCTGCTGCT 656
Db 570 CCGAGACACGACGACCTTCTCTACCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCT 629
Qy 657 TGTCTCTCTCCCGTCT 713
Db 630 GCTTGCACCAATCCCGGCTGCGGTGAGGAGCAAGCGCTTCCGCGGTGCGCGCG 689
Qy 714 TCCCGGCT 773
Db 690 TCTTGCAGATCCGCTCTGCGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 749
Qy 774 TCTTCCCGTCT 833
Db 750 GCTACATGACGATCTCTGCTGCAAGCGAGTGGCTTTCGAGCTTCTCTCTCTCTCT 809

Db	834	TCCTGACTCTCCTCCCGCTCCTCCCGGCTCTGCTCTCCCGATCTCCCGATCTCGTCC	893
Qy	810	CCAACTATATGAGCGTGAATGAGCGCGGTGAACCCGAGCGGACTTATCCGCTTC	869
Db	894	TCCCGTCTCTCCCGTCTCTGCTCTCCCGTCTCCCGTCTCTCTCTCTCTCTCCCGTCTTC	953
Qy	870	GCGGTATCCGCTTCTCCGCGAAGAGGAGGTGCGGAC-----GAAACCTCGCGCGGC	922
Db	954	TCGTCTCTCCCGTCTCTGCTCTCAACCTTCGCGCCCACTCTCTCGTACCTTCGCGGCC	1013
Qy	923	ATCACCGTGAACCAACCGGCGCGTTCCTCTTCCCGGACCTTCGCGGCTTC	973
Db	1014	AGCTCTCTCACTACCTCTCGGCGCCAGACTCTCTCACTACCTTCGCGGCGGCC	1064

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1      RESULT 14
2      US-09-130-114-2
3      : Sequence 2, Application US/09130114
4      : Patent No. 5976807
5      : GENERAL INFORMATION:
6      : APPLICANT: Horlick, Robert A.
7      : APPLICANT: Dama, Bassem B.
8      : APPLICANT: Robbins, Alan K.
9      : TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
10     : FILE OF INVENTION: From Multiple Transfected Episomes
11     : FILE REFERENCE: 0867/11903US1
12     : CURRENT APPLICATION NUMBER: US/09/130.114
13     : CURRENT FILING DATE: 1998-08-06
14     : NUMBER OF SEQ ID NOS: 36
15     : SOFTWARE: FastSeq for Windows Version 3.0
16     : SEQ ID NO 2
17     : LENGTH: 1931
18     : TYPE: DNA
19     : ORGANISM: EBNA
20     : US-09-130-114-2

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Query Match	14.0%;	Score 137;	DB 2;	Length 1931;
Best Local Similarity	48.8%;	Pred. No. 3.4e-15;		
Matches 464;	Conservative 0;	Mismatches 475;	Indels 12;	Gaps 3;

QY	32	ACCTCAACCAAGACACATCTGCGGCTCTTCGCGGACTTTCCTCCGCGCTGACCGGAG	91
Db	117	ACCTGCTCTCCCTCCCTTCTCCTCTGCTCTGCTCTCTCCGCTTCTGAGTCTCCGCGGACCCGAC	176
QY	92	TTCTTCGAGCTCCCGCAAGGCCCTCGCCGAGAGGCGCGCGGCTCTCGCGCGGCGCGG	151
Db	177	GAGTCTTAGTCTCCGGTTCTGTATCTCTACACAGGACCTCTGGGGTTTTTGCAAGTTCAAC	236
QY	152	GCCGCGGCGGTGCGCACATGTTGACGTGTCCAC - CTTCGACATCGACCGGACGCT	209
Db	237	GTAACCGACGTTTCCCTGGGATGCACCTTGTCTCTGCTCTGCTCCGCTCCGCTCCGCTCCGCTCC	296
QY	210	CCCTCTGACGAGGATGCCGCGCGCGGACAGTCACATCATGTGACCGGCAACCGGCTCT	269
Db	297	TGCTCTCTCCGCTCTCTGCTCTCTCTCCCGTCTGTGCTCTCTCCCGTCTCTCCCGTCT	356
QY	270	GATTGACCCGCGCTCTCAATGCGCTTCGCTCCGTGAGAGAGCTCAACCAATTCTTCC	329
Db	357	TCCCGTCTCCCGCTCTCTGCTCTCTCCCGTCTGCTCTCTCTCCCGTCTCTCCCG	416
QY	330	TCCGCGAATCCAGTACGAGCATTCGAGACACCGGATCCGCGCGGACTATCAAGTGG	389
Db	417	TCTCTCCCGTCTCTGCTCTCTCCCGTCTGTGCTCTCTCCCGTCTCTCCCGTCTCTG	476
QY	390	CCACCACTGGCAAGGCCAACCCTGTTCCAGAGCTGTGCTCAAGGCGCGCGCGCGCT	449
Db	477	TCTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTGCTCTCTCTCCCGTCTGCTCTCTC	536
QY	450	CCCTTCGACACGCGGCTGCGGATCCACACACCGCGCTCCGAGGCGACGCGGACG	509
Db	537	TCCCGTCTCTCCCGTCTCTGCTCTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTGCTC	596
QY	510	AGCAGGCGCATCTTGAATTCGAGGCGCTTCCCGTCCCGCGTGTGATCGGACACT	569

[illegible]

RESULT 15
 US-08-403-852D-4
 : Sequence 4, Application US/08403852D
 : Patent No. 5891695
 : GENERAL INFORMATION:
 : APPLICANT: Blanc, Veronique
 : APPLICANT: Blanche, Francis
 : APPLICANT: Crouzet, Joel
 : APPLICANT: Jacques, Nathalie
 : APPLICANT: Lacroix, Patricia
 : APPLICANT: Thibaut, Denis
 : APPLICANT: Zagorec, Monique
 : APPLICANT: Debussche, Laurent
 : APPLICANT: De Crecy-Lagard, Valerie
 : TITLE OF INVENTION: Polypeptides Involved In The
 : TITLE OF INVENTION: Biosynthesis Of Stereogammas, Nucleotide Sequences
 : TITLE OF INVENTION: Coding For These Polypeptides And Their Use
 : NUMBER OF SEQUENCES: 43
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett & Dunner
 : STREET: 1300 I Street, N.W., Suite 700
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20005-3315
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/403,852D
 : FILING DATE: 10-MAY-1995
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: PCT/FR 93/00923
 : FILING DATE: 25-SEP-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: FR 92/11441
 : FILING DATE: 25-SEP-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 03806.0054-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1208 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *S.pristinaespiralis*
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1208
 US-08-403-852D-4

Query Match 11.3%; Score 110.8; DB 2; Length 1208;
 Best Local Similarity 47.1%; Pred.No.1.1e-10;
 Matches 469; Conservative 0; Mismatches 497; Indels 30; Gaps 3;

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QY 13 CATCTCGAGCGCGGCTTCAACCTTCAACGAGCAGCATCTGGGCTCTCCGCGGCTT 72
DB 18 CACCTTCGAGTCTCGTACGAGGCGCCACCCGACAGATCGCCGACAGATCAGTACAC 77
QY 73 CTTCCGCGCTTGGAGGCTTCTTCCGCTCCCGCAAGGCTTCCGCGAGAGGCGCTGG 132
DB 78 CGTCTCGACGCGCTGCTGCGAGAGACCCGCTTCAAGCGCTGCGAGTCAAGCTGAT 137
QY 133 CGGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 192
DB 138 CACCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197
QY 193 CATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 252
DB 198 CCAACTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 257
QY 253 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 312
DB 258 CGGCGCGCTCTCGCGCGCTCTCGCTCTCATCGCGCGCGAGTCCCGGACATCGCC 317
QY 313 GCTTACCGAGTTCT-----TCTCTCGCGAGATCCAGTACGGCATCGAGCAC 360
DB 318 CGTTCGACGCGCTTACGAGACCGCGCTCGAGGCGCGAGCGAGCGAGCTGACGAG 377
QY 361 CGGCAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB 378 CGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 437
QY 421 GCTCTGCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 438 GCTGCGCATCGAGCTCGGCCACCGGCTTCCGCGCGCGCGCGCGCGCGCGCGCG 497
QY 481 CACCGCGCGCTTCCGAGCGCGAGCGGCGAGCGAGCGCGCGCGCGCGCGCGCGCG 540
DB 498 CACCGTCCCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 557
QY 541 CTCCCGGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 588
DB 558 CGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 617
QY 589 CTCTTACCTTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 648
DB 618 CGGCTTCCCTGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 677
QY 649 CTCCGCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 708
DB 678 CGCCGAGGCGCGCATCAAGCTCGAGCGAGCAACTACCGCGCTGCTGCTCAACCG 737

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QY 709 GCAGACCGCGCGCGCTCTCTCATCAAGGCGCGCTCATCGACCGAGGCTATGAGCAGATCCT 768
DB 738 CGGTTTCAGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 797
QY 769 CGTGTTCACGACTGCGCTCTTCCGCTTCTCTCTAGCTGACCAACATCATGAGAGTGA- 827
DB 798 CGACAGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 857
QY 828 -----TGACCGCGCGGACCGCGGATGAGGCTTCAATCCCGCTCCGCGTATCCGCT 882
DB 858 CAAAGTCAACGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 917
QY 883 CTTCGCGAGAGAGCGCGCTGCGCGCAGAGACCTTCGCGCGCATCAACGAGCAACCGCGC 942
DB 918 GGGCGCTGCGCTCCGCGCTGCGAGGTCAAGTGGCTTACGCGCATTCGCGCAAGAGCGCG 977
QY 943 CCGCTTCTCTTCCCGACCTTCGCGCGCTCTCTGAGT 978
DB 978 CGGCTGTTCGTCGAGAGCTTCGCGACCGCGCACCGT 1013

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Search completed: February 12, 2005, 05:36:32
 Job time: 172 secs

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